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OM nucleic - nucleic search, using sw model

Run on: July 2, 2005, 12:52:35 ; Search time 514 Seconds
(without alignments)
10206.037 Million cell updates/sec

Title: US-10-047-855-4
Perfect score: 3206
Sequence: 1 gtcgaccacgcgtccggc.....aaaaaaaaaaggcgccgc 3206

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	68.4	2.1	1180	4	US-09-270-767-27552
C 2	68.4	2.1	2786	4	US-09-270-767-11893
3	59.6	1.9	665	2	US-08-883-795A-36
4	57.8	1.8	187169	4	US-09-949-016-12776
5	57.8	1.8	191569	4	US-09-949-016-15940
6	57.2	1.8	1141	4	US-09-806-708B-22
7	54.8	1.7	3042	3	US-09-255-829-17
8	54	1.7	832	4	US-09-621-976-2813
9	53	1.7	88490	4	US-09-949-016-12758
10	53	1.7	88736	4	US-09-949-016-14222
11	52	1.6	3404	4	US-09-710-279-4346
12	51.6	1.6	1987	4	US-09-350-756-8
13	51.6	1.6	2613	3	US-09-255-829-7
14	51.6	1.6	2616	3	US-09-255-829-1
15	51.6	1.6	2622	3	US-09-255-829-25
16	51.6	1.6	2622	3	US-09-255-829-5
17	51.6	1.6	2628	3	US-09-255-829-9
18	51.6	1.6	2637	3	US-09-255-829-11
19	51.6	1.6	2685	3	US-09-255-829-3
20	51.6	1.6	2724	3	US-09-255-829-15
21	51.6	1.6	2862	3	US-09-255-829-13
22	51.6	1.6	3891	1	US-08-480-604A-27
23	51.6	1.6	3891	2	US-08-405-496A-27
24	51.6	1.6	3891	3	US-08-915-136-27
25	51.6	1.6	3891	4	US-09-084-517-27
26	51.6	1.6	4835	4	US-09-288-326A-10
C 27	51.4	1.6	12313	4	US-09-949-016-13248

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ALIGNMENTS

RESULT 1

US-09-270-767-27552/c
; Sequence 27552, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27552
; LENGTH: 1180
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-27552

Query Match 2.1%; Score 68.4; DB 4; Length 1180;

Best Local Similarity 44.7%; Pred. No. 1.2e-07;
Matches 409; Conservative 0; Mismatches 491; Indels 16; Gaps 3;

QY	978	CAGAAATTC	CGGAAACA	AATAGCAAGT	GAGAGTTG	ACTATATA	TATATTAAG	CCATT	1037
DB	920	CAAGATG	CAGATG	AGACCC	TGGCCAGG	CTGAGG	CTTCCCTAT	TGCGG	861
QY	1038	ACCAGGAT	ACAGTT	TGTGACAT	GAAATCTT	CAATTTT	TCCAAGT	ATTGGA	1097
DB	860	CGGTACT	CGCGCG	TAGACTT	CAAGAAC	CACTAT	GTCTACT	TGCGC	801
QY	1098	ATTGGAT	TGGCCAT	CGAGTG	CAGGAA	CTCTAC	AACTCC	CCAGCT	1157
DB	800	CAACCTG	GATGGG	TATCAT	CGTGAAT	GGAAGT	TACATT	GCAGC	741
QY	1158	TCAAGAA	ATACTAT	TGCTTCTT	TAAAGAA	TGCTAG	TATCAT	GTG	1217
DB	740	AAGGAG	AACACT	ATCGG	CTTCTT	CTGAGG	CCCATG	AACAT	681
QY	1218	ATTGAGT	ACACCT	TTTCAAG	GACTTT	TGCGCG	TGATAT	CATGAT	1277
DB	680	GTTGGAT	GCTCAT	TGCTGAT	GGTGGT	GTGCTG	TATAT	CACGAT	621
QY	1278	TTTGACT	ATGAAA	AGAAAT	TTTGAT	GCTGAT	CCAGT	TGAAAT	1337
DB	620	AACTGCT	CCCGCT	CGCAAG	CAGATC	AGCCG	CCAGAC	GAGT	561
QY	1338	AGAATTA	CACTTT	GACCACT	CCAGT	TGTTAA	AGCTACT	CATG	1397
DB	560	AGACATA	AACTAT	GAGT	GTCTCA	AAAGG	CTCGG	CACTT	501

C	28	51	1.6	1141	4	US-09-806-708B-22	Sequence 22, Appl
	29	50.4	1.6	2421	4	US-09-248-796A-1858	Sequence 1858, Ap
	30	50.4	1.6	6124	3	US-08-213-419B-3	Sequence 3, Appl
	31	49.4	1.5	119153	4	US-09-949-016-12378	Sequence 12378, A
	32	49.2	1.5	108310	4	US-09-949-016-16366	Sequence 16366, A
	33	49	1.5	601	4	US-09-949-016-156535	Sequence 156535,
	34	48.6	1.5	29717	4	US-09-949-016-16284	Sequence 16284, A
	35	48.6	1.5	60376	4	US-09-949-016-12423	Sequence 12423, A
	36	48.2	1.5	251672	4	US-09-949-016-17296	Sequence 17296, A
	37	48.2	1.5	251682	4	US-09-949-016-11973	Sequence 11973, A
	38	47.8	1.5	231129	4	US-09-949-016-16110	Sequence 16110, A
	39	47.8	1.5	266293	4	US-09-949-016-11934	Sequence 11934, A
	40	47.4	1.5	9447	4	US-09-949-016-14649	Sequence 14649, A
	41	47.4	1.5	50383	4	US-09-949-016-17600	Sequence 17600, A
	42	47.2	1.5	601	4	US-09-949-016-54020	Sequence 54020, A
	43	47.2	1.5	601	4	US-09-949-016-54021	Sequence 54021, A
	44	47.2	1.5	601	4	US-09-949-016-54024	Sequence 54024, A
	45	47.2	1.5	601	4	US-09-949-016-108654	Sequence 108654,

Qy 1398 TAAGATCGGAAGAATCTGTGGTTTCAGGAGGAAAATTCCTTTTCAGAAAATCAGCCATT 1457
| | | | |
Db 500 GAGGAG-----TATCCCTCGCACACAGCCGAGCCAGATGGAACACCGCATATT 450
| | | | |
Qy 1458 TCCCTTCCTTA-AGATGGTTTACAGTCTTTGCGCAGAAAGATGTAGGGTTTAAACATTTGAAA 1516
| | | | |
Db 449 CCCAACGCTGGTTGAGGATCTGAGAAAGCTGCCCAAGTCACTGGGCATTGATGTGGAGA 390
| | | | |
Qy 1517 TAAATGGATCGCCAGCAAGGATGGAATGTGGGATGTAACTTATCAACATATTTTG 1576
| | | | |
Db 389 TTAAGTGGCCACAGCGTCGCCAGGCGGAGGATCAGAGGCTGAGCAACAA-----TCG 336
| | | | |
Qy 1577 ACATGAATCTGTTTGGATATAATTTTAAAACTGTTTAAAGAAATTCCTGGGAAGAGGA 1636
| | | | |
Db 335 ACAAGAACTTCTCGCCGACAGGTGATCCATCAGGTGATCCAGAGGGCTGTGGCAGAC 276
| | | | |
Qy 1637 GAATAGTCTTTTCTTCATTTTCATGACAGATATTTGCAATGTTTCGCGCAAAAAGCAGAAACA 1696
| | | | |
Db 275 CGATAATCTTCTCGAGTTCGATGCTGACATGTGACGATGCTGAGGTTCAAGCAGAAACG 216
| | | | |
Qy 1697 AATATCCGATACTATTTTAACTCAAGGAAAATCTGAGATTTATCCTGAACTCATGGACC 1756
| | | | |
Db 215 TCTTCCAGTGTGTTCTCAGCAGGAGAGACGAAAGTGGCAGCGGTTCTCTGGATC 156
| | | | |
Qy 1757 TCAGATCTCGGACAAACCCCATTCGAATGAGCTTTGCACAGTTTGAATACTACTGGGGA 1816
| | | | |
Db 155 TCGCAACACGAGACCTTTATTGCGCCGTAATAAATAATGCTCAAGCTTTCGAGCTGGCTGGCA 96
| | | | |
Qy 1817 TAAATGTACATCTCAAGACTTGTCTCAGAAACCCATCTATATTTCAAGAGGCAAAAGCTA 1876
| | | | |
Db 95 CAGCTCCACACGCCGAGACTTCTTGGCGGAAATGCAATCAGAAATGCTCGGAAAGCCA 36
| | | | |
Qy 1877 AGGACTAGTCATATT 1892
| | | | |
Db 35 AGGATCTGGCCAAAT 20
| | | | |

RESULT 2
US-09-270-767-11893/c
; Sequence 11893, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11893
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11893

Query Match 2.1%; Score 68.4; DB 4; Length 2786;
Best Local Similarity 44.7%; Pred. No. 1.9e-07;
Matches 409; Conservative 0; Mismatches 491; Indels 16; Gaps 3;

Qy 978 CAGAAATCCCGAAAACAAATAGGCAAGTGAGAGTTGACTATATATTTTAAAGCCATT 1037
| | | | |
Db 1895 CAAGAATCGAGATGAGACCCCTGGCCAGGCTGAGGCTTCCCTATGTGCGGTCGAGCCCTTA 1836
| | | | |
Qy 1038 ACCAGATACAGTTGTGACATGAATCTTCATTTTCCAAAGTATTTGAAGCCCAAGAAATACC 1097
| | | | |
Db 1835 CCGCTACTCGCCGCTAGACTTCAGAACACCTAATGCTACTGCTGCCCCAAGAGCTGGCC 1776
| | | | |
Qy 1098 ATTGGATGTGGCATCGAGGTGAGGAACTCTCAACAACCTGCCAGCTGGCTAAAGT 1157
| | | | |
Db 1775 CAACCTGGATGTGGTCATCTGTGAAATGCAAGAGTTACATTGACAGCGCTCTCGCGGA 1716
| | | | |
Qy 1158 TCAAGAAAATPACTATTCTTCTTTAAGAAATGCTGCTAGTCATGTTGCGAGCCTTTGTAGA 1217
| | | | |

Db 1715 AAGGAGAACACTATTCGGTCTTCTCTGAGCGCCCATGAACATCAGCAGACATGATCGA 1656
| | | | |
Qy 1218 ATTTGACGTACACCTTTTCAAAGGACTTTTGTCCCGTGGTATATATCATGATCTTACTGTTG 1277
| | | | |
Db 1655 GTTGATGTCCATTGACTGCTGATGGTGTGCTGTGATTTATCAGGATTTCCGACTGCG 1596
| | | | |
Qy 1278 TTTGATATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTCAGTTAAA 1337
| | | | |
Db 1595 AACTCTCGCCTGGCAAGCAGATCAGCGGCCAGACCCAGCTGGAGTACGTGCTGATCAA 1536
| | | | |
Qy 1338 AGAATTAACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATC 1397
| | | | |
Db 1535 AGACATAAATATGAGCTGCTCAAAGGCTGCGCATCTCTGTGATCGCAGGCCAAGT 1476
| | | | |
Qy 1398 TAAGATCGGAAGAATCTGTGGTTTCAGAGGAAAAATTCCTTTTCAGAAAAATCAGCCATT 1457
| | | | |
Db 1475 GAGGAG-----TATCCCTCGCAACAAGCCAGCCAGGATGGAACACCGCATATT 1425
| | | | |
Qy 1458 TCCCTTCCTTA-AGATGGTTTTCAGTCTTTGCGCAGAAAGATGTAGGGTTTAAACATTTGAA 1516
| | | | |
Db 1424 CCCAAGCTGGTTGGAGTACTGGAGAAAGTGTCCCAAGTCACTGGGCTTGTATGTGGAGA 1365
| | | | |
Qy 1517 TAAATGGATCTGCCAGCAAGGATGGAATGTGGGATGTTAACTTATCAACATATTTTG 1576
| | | | |
Db 1364 TTAAGTGGCCACAGCGTTCGCCAGGCGGAGGATCAGAGGCTGAGCAACAA-----TCG 1311
| | | | |
Qy 1577 ACATGAATCTGTTTTCGATATAATTTTAAAAAATCTGTTTTCAGAAAAATTCGGAAGAGA 1636
| | | | |
Db 1310 ACAAGAACTTCTTCCGCGCAAGGTGATCCATCAGTGTATCCAGAGGCTGTGGCAGAC 1251
| | | | |
Qy 1637 GAATAGTGTCTTCTTCATTTGATGACAGATATTTGCAATGTTTCGCGCAAAAGCAGAAACA 1696
| | | | |
Db 1250 CGATAATCTTCCAGCTTCGATGCTGACATGTGACGATGCTGAGGTTCAAGCAGAAACG 1191
| | | | |
Qy 1697 AATATCGATATATTTTAACTCAAGGAAATCTGAGATTTATCTGAATCATGAGCC 1756
| | | | |
Db 1190 TCTTCCAGTGTGTTCTCTCAGCAGGAGAGACGAAAGATGGCAGCGCTTCTCTGGATC 1131
| | | | |
Qy 1757 TCAGATCTGGCAACCCCATTCGAATGAGCTTTGCAAGTTTGAATAATCTACTGGGGA 1816
| | | | |
Db 1130 TCGCAACAGCGACCTTTTATTCAGCGCTTAACAATGCTCAAGCTTTCGAGCTGGCTGGCA 1071
| | | | |
Qy 1817 TAAATGTACATCTCAAGACTTGTCTCAGAAACCCATCTTATATTCAGAGGCAAAAGCTA 1876
| | | | |
Db 1070 CAGCTCCACAGCGCGAGGACTTCTTCTGGCGAAAAATGCAATCAGAAATGCTCGCAAAAGCCA 1011
| | | | |
Qy 1877 AGGACTAGTCATATT 1892
| | | | |
Db 1010 AGGATCTGGGCCAAAT 995
| | | | |

RESULT 3
US-08-883-795A-36
; Sequence 36, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: Rh 32
US-08-883-795A-36

Query Match 1.9%; Score 59.6; DB 2; Length 665;
Best Local Similarity 47.1%; Pred. No. 1.9e-05;

Matches 214; Conservative 0; Mismatches 239; Indels 1; Gaps 1;

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QY 2212 TATTCATTTTTCATCACTGAGCATTGTCATCTATGCGCTTTGGGCTTCAGTTCATG 2271
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Db 66  TATTTATAATTAAATATTTTATAATTAAATATTTATAATTAAATATTTATAATTAA 125

QY 2272 AAGCAATAATGAAGTATTTAACTCTTTCACTA-CAGTCTTCGCAAGTATGCTATTTAAAT 2330
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 TATTTATAATTAAATATTTTATAATTAAATATTTATAATTAAATATTTATAATTAA 185

QY 2331 TACTTGGCCAGGTAAATGCGCAGTCCTTTATAGTGAAGAAATTTATGTTAGT 2390
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 TATTTATAATTAAATATTTTATAATTAAATATTTATAATTAAATATTTATAATTAA 245

QY 2391 AATATAAATATTTTAACTAAATATATAAATCTATAATGCTTAAACATATGTTCAATAAA 2450
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 TATTTATAATTAAATATTTTATAATTAAATGTTTATAATTAAATATTTATAATTAA 305

QY 2451 GCATAGCACTTTGAAATTAACATATATAAATAGCTCATATTTACACTACAGCTTTTCAT 2510
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 TGTTTATAATTACATATTTTATAATTAAATGTTTATAATTACATATTTTATAATTAA 365

QY 2511 TGATCAGGTCTGAATCTTTAGCACTTAAGGAAATGACTATGCATAATTACCTGACC 2570
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 TGTTTATAATTACATATTTTATAATTAAATGTTTATAATTACATATTTTATAATTAA 425

QY 2571 ATGAAAAAATAAGTACCTCAATGCATGCAATTCGACCTGGTGATTCCACTGCACAAT 2630
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 TGTTTATAATTACATATTTTATAATTACATATTTTATAAAGTATTTATAATTACATAT 485

QY 2631 CTTTGTGCCATCTTGTATATAGTATTTTATTTTACA 2664
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 TATAATTAAAGTATTTATAATTACATATTTTATA 519
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RESULT 4

US-09-949-016-12776
Sequence 12776, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12776
LENGTH: 187169
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(187169)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776

Query Match 1.8%; Score 57.8; DB 4; Length 187169;
Best Local Similarity 43.6%; Pred. No. 0.0012;

Matches 257; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

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QY 2361 TCTTTATAGTCGAGAAATTTTATGTTAGTAAATATTTTAAACTAAATATATAA 2420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 624 TATATAATATAAATAATATAATATAATATAAATAATATAAATAATATAAATAAT 683

QY 2421 TCTATAATGTTTAAACATATGTTTCAATTTAAAGCATAGCAGCTTTGAAATTAAC 2480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 684 ACATAAATAATATAAATAATATAATATAAATAAATAAATAATATAAATAATATAA 743

QY 2481 AGCTCATATTTACACTTACAGCTTTTCATTTGATCAGGCTCGAAATCTTTAGCACT 2540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 744 AAAATATAAATAATATAAATAATATAAATAAATAAATAATATAAATAAATAAATA 803

QY 2541 GAAATGACTATGCTAATATATACCTGACCATGAAATAAATAAGTCACTCAATGCGAT 2600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 804 ATATATAAATAATATAAATAATATAAATAAATAAATAAATAAATAAATAAATAAATA 863

QY 2601 ATTTGCACTGCTGATTTCCAACTGCACAAATCTTTTGCCATCTTGTATATAGTATTT 2660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 864 AATATAATAAATAATATAAATAATATAAATAATATAAATAAATAAATAAATAAATA 923

QY 2661 TACATGGTTCACATGACACACACACATTTTCATTCAGTATGAACTTTGAGGCTGCTGC 2720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 924 TATAATATAAATAAATAAATAATATAAATAAATAAATAAATAAATAAATAAATAAATA 983

QY 2721 CATTTTCCACTTAAACCAACACGCTGAAGTCACTCGAACTTGTTCATAAATCT 2780
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 984 TGATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1043

QY 2781 TTCAAAAGTTGTTTTACATCAATGTTAAAAATTTCAAAATGCTGCAGGTAATTTAAATG 2840
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1044 TATATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1103

QY 2841 TAAATAATTTAGTAAAGAAAAAGTATGTTATGTCATCTTAGTAGAATAGATCAACATACA 2900
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1104 TATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1163

QY 2901 AATTCAATTGCTGATGCTTTAGTCTTAAGCATGAGATTGTACATGT 2949
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1164 TAATACATATAATTTATATATATTTATATAAATAAATAAATAAATAAATAAATAAATA 1212
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RESULT 5

US-09-949-016-15940
Sequence 15940, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15940
LENGTH: 191569
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(191569)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15940

PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAEl promoters
US-09-806-708B-22

Query Match 1.8%; Score 57.2; DB 4; Length 1141;
Best Local Similarity 11.2%; Pred. No. 0.00011;
Matches 121; Conservative 395; Mismatches 556; Indels 11; Gaps 3;
QY 1841 TCAGAAACCCATCTATATTCAAGAGGCAAAAGCTAAGGAGCTAGTGCATATTCGTCTGGG 1900
DB 60 TWARMYCKYRRYNNKSRWKGWYKKYBNCANNTSBRVHARRWKDKMTAYBMTWTKWG 119
QY 1901 GTGATGATACCAATGATCTCGAAAAACAGAGGAATTTGAAGAACTTGGAGTTAATGGTC 1960
DB 120 KTCGRHRYWRWAMBDVDHYYVTAMNNATWTCMMDKDDKTRWKKNNATGDDDT 179
QY 1961 TAAATTTATGATGATATATGATGCTGCAACCAACCAATATATTCAGTGGAGC 2020
DB 180 KYHMNNNGCBVTVMVRYKTDSDSKRMNKGMBWKNWSDYDVTYVWVDDMCKRKYR 239
QY 2021 AATTGGAACCCCTGAAGCAGGAAATTCAGAGCTTAAGAGCTGTTGTGTCCACATGTTA 2080
DB 240 RWVRTGRMKNYVWABTAHRRYNNGTBAMAYRWTWNNNNNNNAKMKRAKYWGNR 299
QY 2081 GCGCGTTTGTCCCTCATCTTTGTGTGGGAGTCTGATATPCCATG--TGGATGCCAACGG 2138
DB 300 ABVNSTCTTKWSKTTKVRTSWANNCRAGDANKDKHWKWSAAMGVYNNNNNNNTYK 359
QY 2139 CATGTATAACCTGGAGATGCTTAGTTTATGACAGAGGTCATTTTGGGGCGCTGCA 2198
DB 360 ARHBAHDWYHSAWKWANAHAHYSRKKWBTBVTWNNNNNGTTWKKMWAHYWKMDM 419
QY 2199 CCGCTGTCTGGGTATTCACTTTTTCATCTAGCAGCATTTGTGATCTATGCTTTTGGCT 2258
DB 420 DWBGTYNNNGRTYYGWTGNKWKWYKWKANNCKRAWDHKTCTHNNTTWKKWY 479
QY 2259 TCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTTCTACATGTTCTTGCAGTA 2318
DB 480 NNCYKSWTNGKSHRBAAAVVYTWMMWRRYAHANNNNNDYMWKACTWYKYBVCYKSWNN 539
QY 2319 TGCTATTAAATTTACTTGGCCAGGTATAATGCCAGTCAGTCTCTCTTTTATAGTGAGAAAAT 2378
DB 540 YAAWYTKSNNYTSRYRWTNNNSWRWSDTRSGRANNYARABHY----GYKNWTRWB 595
QY 2379 TTATTGGTTAGTATAATAATATTTTAACTAAATATAATAATCTATAATGTTTAAACATA 2438
DB 596 WSHTWBHRAGAHHYHMBMYBAKCHCKAWYKAKYAGAGSNNNNNNNNNNNNNNNNNA 655
QY 2439 TGTTCATTAAAGCATAGCCTTTTGAATAATAACTATATAAATAGCTCATATTTACACTTA 2498
DB 656 TCARDYYAASRWYMANAKWYKBAANNAYYTHANNWGCWNNATDTRRTWKKNNNN 715
QY 2499 CAGCTTTTCTGATCAGTCTGAAATCTTTAGCAGCTTAAGGAAATGACTATGCATAA 2558
DB 716 NAGTWKNNNNNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAKNAK 775
QY 2559 TTATACCTGACCATGAAATAAATAAGTACCTCAATGATGATGCTTGTGCTGCTGCTCC 2618
DB 776 AYTCTTTNNNTYRGVVVNTAARDGWANNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 835
QY 2619 AACTGCACAAATCTTTGTGCGCATCTTGTATATAGGTATTTTTCATGCGGTTGATGCA 2678
DB 836 NNNNNNNNNAYAWWTKWYTTDDWRBAYTTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 895

Query Match 1.8%; Score 57.8; DB 4; Length 191569;
Best Local Similarity 43.6%; Pred. No. 0.0012;
Matches 257; Conservative 0; Mismatches 332; Indels 0; Gaps 0;
QY 2361 TCTTTATAGTGAGAAATTTATTGGTTAGTATAATAATTTTAAACTAAATATATAA 2420
DB 624 TATATAATATAAATAATATAATAATATAATAATAATAATAATAATAATAATAATAT 683
QY 2421 TCTATAAATGTTAAACATATGTTTCATTAAGCATAGCAGCTTTGAAATTAACATATAAAT 2480
DB 684 ACATAAATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 743
QY 2481 AGCTCATATTTACATCTACAGCTTTTCATTTGATCAGCTCTGAATCTTTAGCATTAG 2540
DB 744 AAAATATAAATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 803
QY 2541 GAAATGACTATGCATATATACCTGACCAATGAAATTAAGTACCTCAATGCATGC 2600
DB 804 ATATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 863
QY 2601 ATTTCACCTGGTGATTCACACTGCACAAATCTTTGTGCCATCTTGTATATAGTATTTT 2660
DB 864 AATATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 923
QY 2661 TACATGGGTGATGACACACACACCAATTTTCATTCAGTATGAACTTGGCTGCTGC 2720
DB 924 TATAATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 983
QY 2721 CATTTTCACCTAACCAACAGCTGAGGTGACCTCGAACTTGTTCATAAACT 2780
DB 984 TGATATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1043
QY 2781 TTCAAAAGTTGTTTACATCAATGTTTAAATTTTCAAAATGCTGCAGGGTAATTTAATGTA 2840
DB 1044 TATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1103
QY 2841 TAAATATTTAGTAAGAAAAGTATGTTTGCATCTTACTAGTAGAATAGATCAACATACA 2900
DB 1104 TATAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 1163
QY 2901 AATTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAGATTTGATCATGT 2949
DB 1164 TAATACATATATATTAT 1212

RESULT 6
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806, 708B
CURRENT FILING DATE: 2001-04-03


```
; LENGTH: 3404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4346

Query Match
Best Local Similarity 1.6%; Score 52; DB 4; Length 3404;
Matches 139; Conservative 0; Mismatches 105; Indels 4; Gaps 2;

QY 2342 GTATTAATGCCAGTCAGTCTCTTTATAGTCAGAAATTTATTTGGTAGTATATAATAT 2401
DB 416 GAAATAATTAAGATCAAAATCTTAATATGTTGTAATTTAATGGTACCTAAAAATAAAA 475
QY 2402 TTAAACTA-RATATATAATCTATAATCTTAAACATATGTTCAATAAA--GCATAGC 2457
DB 476 TTAAACTACAAATGCTAAATCCATATGTTGTTTCATTAGAGATTTAAATAATGATTATA 535
QY 2458 ACTTTGAAATTAACATATATAATAGCTCATATTTACACTTACAGCTTTTTCATTTGATCAG 2517
DB 536 ACACATAAAGATTTCAAATATTATATTTAATATAAATTTACATATGATAACGAATAAC 595
QY 2518 GTCTGAATCTTTAGCAGCTTAAGGAAATGACTATGCATATATATACCTGACCATGAAAA 2577
DB 596 AATTCCTAATAAATTTATTTTGTGATTTATTTTATTAATACTATATATTTATATGAAAA 655
QY 2578 AATAAGT 2585
DB 656 ATATAAGT 663

RESULT 12
US-09-350-756-8
; Sequence 8, Application US/09350756
; Patent No. 6495143
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research Institute for Infectious Diseases
; APPLICANT: John S. Lee
; APPLICANT: Peter Pushko
; APPLICANT: Michael D. Parker
; APPLICANT: Jonathan P. Smith
; APPLICANT: Mark T. Dertzbaugh
; APPLICANT: Leonard Smith
; TITLE OF INVENTION: Botulinum Neurotoxin Vaccine
; FILE REFERENCE: 003/124/SAP R11D 98-21
; CURRENT FILING DATE: 1999-07-09
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 1987
; TYPE: DNA
; ORGANISM: Clostridium botulinum
; FEATURE:
US-09-350-756-8

Query Match
Best Local Similarity 1.6%; Score 51.6; DB 4; Length 1987;
Matches 151; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 2258 TTCTCAGTTCATGAAGCAATTAATGAAGTATTTAACTCTTTCACCTACAGTCTTTCAGT 2317
DB 1011 TTCGAACTTAATGAGTCTCTATAAATAAAGCTATGATTAATAATAAATTTTGAATCA 1070
QY 2318 ATGCTATTAAATTAATTTGCGCCAGGTATAATTTGCGAGTCAGTCTCTTTATAGTGAGAAA 2377
DB 1071 ATGCTCTGTTTCATATTTTAATGAATCTTATGATCCCTTATGGTGTAAACGGTTAGAAGA 1130
QY 2378 TTTATTTGGTTAGTATAATAAT---ATTTTAACTAAATATAATAATCTATAATGTTAAA 2434

; LENGTH: 3404
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4346

Query Match
Best Local Similarity 1.6%; Score 52; DB 4; Length 3404;
Matches 139; Conservative 0; Mismatches 105; Indels 4; Gaps 2;

QY 2342 GTATTAATGCCAGTCAGTCTCTTTATAGTCAGAAATTTATTTGGTAGTATATAATAT 2401
DB 416 GAAATAATTAAGATCAAAATCTTAATATGTTGTAATTTAATGGTACCTAAAAATAAAA 475
QY 2402 TTAAACTA-RATATATAATCTATAATCTTAAACATATGTTCAATAAA--GCATAGC 2457
DB 476 TTAAACTACAAATGCTAAATCCATATGTTGTTTCATTAGAGATTTAAATAATGATTATA 535
QY 2458 ACTTTGAAATTAACATATATAATAGCTCATATTTACACTTACAGCTTTTTCATTTGATCAG 2517
DB 536 ACACATAAAGATTTCAAATATTATATTTAATATAAATTTACATATGATAACGAATAAC 595
QY 2518 GTCTGAATCTTTAGCAGCTTAAGGAAATGACTATGCATATATATACCTGACCATGAAAA 2577
DB 596 AATTCCTAATAAATTTATTTTGTGATTTATTTTATTAATACTATATATTTATATGAAAA 655
QY 2578 AATAAGT 2585
DB 656 ATATAAGT 663

RESULT 13
US-09-255-829-7
; Sequence 7, Application US/09255829
; Patent No. 6461617
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,829
; FILING DATE: 23-FEB-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/02273
; FILING DATE: 22-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/782,893
; FILING DATE: 27-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ESMOND, ROBERT W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0130002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 2613 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2613
US-09-255-829-7

Query Match
Best Local Similarity 1.6%; Score 51.6; DB 3; Length 2613;
Matches 151; Conservative 0; Mismatches 144; Indels 3; Gaps 1;

QY 2258 TTCTCAGTTCATGAAGCAATTAATGAAGTATTTAACTCTTTCACCTACAGTCTTTCAGT 2317
DB 2310 TTCGAACTTAATGAGTCTATAAATAAAGCTATGATTAATAATAAATAAATTTTGAATCA 2369
QY 2318 ATGCTATTAAATTAATTTGCGCCAGGTATAATTTGCGAGTCAGTCTCTTTATAGTGAGAAA 2377
DB 2370 ATGCTCTGTTTCATATTTTAATGAATTTCTATGATCCCTTATGGTGTAAACGGTTAGAAGA 2429
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2370	ATGCTCTGTTTCATATTTAAATGAAATCTATGATCCCTTATGGTGTTAAACGGTTAGACA	2429
Db		
2378	TTTATTTGGTTAGTAATATAAAAT - - -ATTTTAAACTAAATATATAAAATCTATATGTTTAA	2434
Qy		
2430	TTTGTGCTAGTCTTTAAAGATGCGATTTATTAAGTATATATATGATATATAGAGGAACTTT	2489
Db		
2435	CATATGTTTCATTTAAAGCATAGCACCTTTTGAATTAACATATAAAATAGCTCATATTTTACA	2494
Qy		
2490	AAATGGTCAAGTAGATAGATTAAAAAGATAAAGTTAAATAACACTTAGTACAGATATACC	2549
Db		
2495	CTTACAGCTTTTCATTTGATCAGGTCGAAATCTTTAGCACCTTAAGGAAAAATGACCTAT	2552
Qy		
2550	TTTTTCAGCTTTCCAAATACGTAGATAATCAAAGATTATTTATCTACATTTTCTGTAATAT	2607
Db		

RESULT 15
 US-09-253-829-25
 ; Sequence 25, Application US/09255829
 ; Patent No. 6461617
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Shone, Clifford Charles
 ; APPLICANT: Quinn, Conrad Padraig
 ; APPLICANT: Foster, Keith Alan
 ;
 ; TITLE OF INVENTION: Recombinant Toxin Fragments
 ;
 ; NUMBER OF SEQUENCES: 29
 ;
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
 ; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
 ; CITY: WASHINGTON
 ; STATE: DC

[illegible]

FILING DATE: 25-JUN-1999
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB97/02273
 FILING DATE: 22-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/782,893
 FILING DATE: 27-DEC-1996
 ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-26

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

; LENGTH: 2616 base pairs

```

; STRANDEDNESS: double

```

; MOLECULE TYPE: DNA (genomic)

```

;
NAME/KEY: CDS
LOCATION: 1, 2, 3, 4

```

```

; LOCATION:
; 00 0FF 020 2E

```

Query Match 1.6%: Score 51.6: DB 3: Length 2616;

Query Match	1.00	Score	1.00
Best Local Similarity	50.78%	Pred. No.	0.0051;

Matches	151	Conservative	0	Mismatches	144	Indels	3	Gaps	1
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2258 TTCTCAGTTCAATGAAGCAATAATGAAGTATTTAACTCTTTCACCTACAGTCTTGCAAGT 2317

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2005, 12:38:20 ; Search time 1635 Seconds
(without alignments)
11607.762 Million cell updates/sec

Title: US-10-047-855-4
Perfect score: 3206
Sequence: 1 gtcgaccacgcgtccggc.....aaaaaaaaagggcgccgc 3206

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3206	100.0	3206	4 AAD06010	Human neu
2	3206	100.0	3206	8 ABS56723	Human NAR
3	3206	100.0	3206	12 ADJ57933	Human NAR
4	3166	98.8	3499	5 ADL62788	Human ova
5	3166	98.8	5443	12 ADN05171	Antipsori
6	3166	98.8	5443	13 ADS74320	PRO83903
7	3164.4	98.7	3499	5 ABV29614	Human pro
8	3152.4	98.3	3498	5 ABV23741	Human pro
9	2481.8	77.4	2738	4 AAD06007	Human neu
10	2481.8	77.4	2738	12 ADJ57931	Human NAR
11	2019	63.0	2019	13 ADR40144	Human NAR
12	1803	56.2	1803	4 AAH14905	Human CDN
13	1698.2	53.0	1929	4 AAH44173	Human gly
14	1471.2	45.9	3381	12 ADJ57938	Rat NAR
15	1406	43.9	2477	5 ABA09667	Human bon
16	1376.4	42.9	1978	5 ABA09583	Human bon
17	991	30.9	2393	12 ADJ57947	Rat NAR
18	633.4	19.8	768	4 AAH07671	Human CDN
19	486.4	15.2	546	4 AAS23890	Human ova
20	486.4	15.2	546	5 AAH82447	Human ova

c	21	469.4	14.6	471	6 ABV88538	Human col
	22	444.6	13.9	490	4 AAH12646	Human CDN
	23	427	13.3	427	9 ACH18980	Human adu
	24	414.8	12.9	520	5 ADL42779	Human ova
c	25	365.6	11.4	403	4 AAS24002	Human ova
c	26	365.6	11.4	403	5 AAH82567	Human ova
	27	363.4	11.3	396	5 ADI71235	Human ova
	28	363.4	11.3	396	5 ADL36395	Human ova
	29	326.6	10.2	425	5 ABV35865	Human pro
	30	326.6	10.2	425	5 ABV44927	Human pro
c	31	326	10.2	327	5 ABV15063	Human pro
	32	296.4	9.2	478	6 ABL81385	Human ova
c	33	291	9.1	510	6 ABL79391	Human ova
	34	285	8.9	298	2 AAT24062	Human gen
	35	271	8.5	359	5 ABV05894	Human pro
	36	265.2	8.3	474	4 AAK61234	Human imm
	37	236	7.4	14598	4 AAK80690	Human imm
	38	236	7.4	14598	4 AAK79627	Human imm
	39	208.4	6.5	463	4 AAI12461	Probe #23
	40	208.4	6.5	463	4 ABA54169	Human toe
	41	208.4	6.5	463	4 AAI33815	Probe #25
	42	208.4	6.5	463	4 ABA43713	Human bre
	43	208.4	6.5	463	4 ABA23914	Probe #23
	44	208.4	6.5	463	4 AAK27880	Human bon
	45	208.4	6.5	463	4 AAK02440	Human bra

ALIGNMENTS

RESULT 1
AAD06010
ID AAD06010 standard; DNA; 3206 BP.

AC AAD06010;

DT 31-JUL-2001 (first entry)

DE Human neuronal apoptosis regulated candidate (NARC) 16B DNA.

KW Human; neuronal apoptosis regulated candidate 16B; NARC 16B; cytostatic;
KW chromosome mapping; gene therapy; antisense therapy; lung disorder;
KW central nervous system disorder; apoptosis; spleen disorder; angina;
KW tuberculous; Goodpasture's syndrome; liver disorder; jaundice;
KW infectious disorder; brain disorder; cerebral oedema; gonorrhoea;
KW heart disorder; kidney disorder; glomerulonephritis; testes; virucide;
KW epididymis disorder; skeletal muscle disorder; pancreatic disorder;
KW diabetes; cytoprotectant; immunostimulant; tumour; antiinflammatory;
KW antimicrobial; neuroprotective; gynaecological; ds.

OS Homo sapiens.

FN WO200131007-A2.

XX 03-MAY-2001.

XX 20-OCT-2000; 2000WO-US029132.

XX 22-OCT-1999; 99US-0161188P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Chiang LW;

XX WPI; 2001-308641/32.

XX Rat brain polypeptides, nucleic acids and antibodies, useful for
PT diagnosis and treatment of central nervous system disorders and disorders
PT associated with aberrant apoptosis.

XX Claim 1; Page 148; 161pp; English.

XX The invention relates to human homologues of neuronal apoptosis regulated

CC candidate (NARC) nucleic acid molecules and proteins derived from rat
CC brain and programmed cell death libraries. The nucleic acids of the
CC invention are useful for assaying the presence of a nucleic acid molecule
CC and for chromosome mapping. They are also used in gene therapy and
CC antisense therapy. The NARC sequences are useful for treating central
CC nervous system disorders and disorders involving aberrant apoptosis, for
CC inducing an immune response and for isolating binding partners. Diseases
CC treated include spleen disorders (e.g. tuberculosis and congestive
CC splenomegaly), lung disorders (e.g. adult respiratory distress syndrome,
CC Goodpasture's syndrome and bronchial asthma), liver disorders (e.g.
CC jaundice and hepatic failure), infectious disorders (e.g. viral
CC hepatitis), brain disorders (e.g. cerebral oedema, hypertensive
CC encephalopathy and hydrocephalus), heart disorders (e.g. heart failure,
CC angina and myocardial infarction), kidney disorders (e.g. cysts and
CC glomerulonephritis), testes and epididymis disorders (e.g. gonorrhoea and
CC syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic
CC disorders (e.g. pancreatitis and diabetes). The present sequence is human
CC neuronal apoptosis regulated candidate (NARC) 16B DNA
XX
SQ Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;

Query Match 100.0%; Score 3206; DB 4; Length 3206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGACCCACCGGTCGGGGGAGGACGGAACGGGGGGCGCCGGTACCTCTGCCCGCGGT 60
DB 1 GTCGACCCACCGGTCGGGGGAGGACGGAACGGGGGGCGCCGGTACCTCTGCCCGCGGT 60
QY 61 CTTCTGCTCTCGGGCGGGGGCGGGAGCGGACCTCGGGACTAGCGAACCCGGAGACG 120
DB 61 CTTCTGCTCTCGGGCGGGGGCGGGAGCGGACCTCGGGACTAGCGAACCCGGAGACG 120
QY 121 ACATCATAAATAAATCCATCAGATGACACCTTCTCAGGTGGCTTTGAAATAAGAGGA 180
DB 121 ACATCATAAATAAATCCATCAGATGACACCTTCTCAGGTGGCTTTGAAATAAGAGGA 180
QY 181 ACTCTTTTACAGGAGAGATTTTTCGGATATGTGGAAGCTGTGATGCTTTGGGAAACTGG 240
DB 181 ACTCTTTTACAGGAGAGATTTTTCGGATATGTGGAAGCTGTGATGCTTTGGGAAACTGG 240
QY 241 AATCTCAAAATGCTGTGGCTCTTCTCCAGAGATGACAGGTGGAAGCATGCTATGG 300
DB 241 AATCTCAAAATGCTGTGGCTCTTCTCCAGAGATGACAGGTGGAAGCATGCTATGG 300
QY 301 AAAGCAACCATTTGTTACTCAGTAGAGAGTATCAGTTTCAGTATCGCTACTTCAAAGGGTAC 360
DB 301 AAAGCAACCATTTGTTACTCAGTAGAGAGTATCAGTTTCAGTATCGCTACTTCAAAGGGTAC 360
QY 361 TTTTGTAGAACCAAGACTATCGGTGGTCCATGTCAGTGTGATGTTTCAAGTGGGAGACT 420
DB 361 TTTTGTAGAACCAAGACTATCGGTGGTCCATGTCAGTGTGATGTTTCAAGTGGGAGACT 420
QY 421 CATCTCAACACGAGTCAATAACCCCTTTAGAAAGGAAATTAATTATTTGACGATGGACAA 480
DB 421 CATCTCAACACGAGTCAATAACCCCTTTAGAAAGGAAATTAATTATTTGACGATGGACAA 480
QY 481 TTTGGAAATCAAGTGGTGTGAACTCTGGATTTCTGGATGCTGACATGTGACAGTCTGAA 540
DB 481 TTTGGAAATCAAGTGGTGTGAACTCTGGATTTCTGGATGCTGACATGTGACAGTCTGAA 540
QY 541 ATAAGATTAAGTTGATTAATTCTGAAAAACCTCTGTGTCATTAATCAAGAAAAAATTA 600
DB 541 ATAAGATTAAGTTGATTAATTCTGAAAAACCTCTGTGTCATTAATCAAGAAAAAATTA 600
QY 601 AAAAAATCTAGATTTAGGTGAACTGACATAGAAAGGCTCGAGGAGATGACCATGAT 660
DB 601 AAAAAATCTAGATTTAGGTGAACTGACATAGAAAGGCTCGAGGAGATGACCATGAT 660
QY 661 AGGGTATCTCCCACTGACTCCACAAAATGTCCTAGATGTTGGAGATATCTTAAATAGC 720
DB 661 AGGGTATCTCCCACTGACTCCACAAAATGTCCTAGATGTTGGAGATATCTTAAATAGC 720

QY 721 GACAAATGAGTTCAAGTGCAGGCAATTCACAGCCGGAGTGTGGTTATGGCTTCGACGCTCAT 780
DB 721 GACAAATGAGTTCAAGTGCAGGCAATTCACAGCCGGAGTGTGGTTATGGCTTCGACGCTCAT 780
QY 781 CTTTGGACAGAGTACAGCATACAGATGAGATGGAACAGATTAACCTTGAATTAATCTTTGAT 840
DB 781 CTTTGGACAGAGTACAGCATACAGATGAGATGGAACAGATTAACCTTGAATTAATCTTTGAT 840
QY 841 TTTTTCGAAAGAGATCTCAGTGAGCAGCATGTAGTTTCAGGGTGTAGTCCCTTCCTGGACATGTG 900
DB 841 TTTTTCGAAAGAGATCTCAGTGAGCAGCATGTAGTTTCAGGGTGTAGTCCCTTCCTGGACATGTG 900
QY 901 GGTACAGCTTGTCTCTTATATCCCAATTCCTGAGAGTGGAAAGAGTCTTGGAAATTCCT 960
DB 901 GGTACAGCTTGTCTCTTATATCCCAATTCCTGAGAGTGGAAAGAGTCTTGGAAATTCCT 960
QY 961 ACTTTTCCCATCATGAGCAGAAATTTCCCGGAAAAACAATAGGCAAAAGTGCAGCTTGCATAT 1020
DB 961 ACTTTTCCCATCATGAGCAGAAATTTCCCGGAAAAACAATAGGCAAAAGTGCAGCTTGCATAT 1020
QY 1021 ATAATTTAATTAAGCCATTACCCAGGATACAGTTGTGATCATGAAATCTTCATTTTCCAAGTAT 1080
DB 1021 ATAATTTAATTAAGCCATTACCCAGGATACAGTTGTGATCATGAAATCTTCATTTTCCAAGTAT 1080
QY 1081 TGGAAAGCCAAAGATACCAATTTGGATGTTGGCCATCGAGGTGCAGGAAACTCTACAACACT 1140
DB 1081 TGGAAAGCCAAAGATACCAATTTGGATGTTGGCCATCGAGGTGCAGGAAACTCTACAACACT 1140
QY 1141 GCCCAGCTGGCTAAAGTTCAAGAAAAATCTATTTGCTTCTTTAAGAAAAATGCTCTAGTCAT 1200
DB 1141 GCCCAGCTGGCTAAAGTTCAAGAAAAATCTATTTGCTTCTTTAAGAAAAATGCTCTAGTCAT 1200
QY 1201 GGTGAGCCTTTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTTGTGCGCGGTGATAT 1260
DB 1201 GGTGAGCCTTTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTTGTGCGCGGTGATAT 1260
QY 1261 CATGATCTTACCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCAGTTGAAATTA 1320
DB 1261 CATGATCTTACCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCAGTTGAAATTA 1320
QY 1321 TTTGAAATTCAGTAAAAAGATTAACATTTGACCAACTCCAGTTGTTAAAGTCACTCAT 1380
DB 1321 TTTGAAATTCAGTAAAAAGATTAACATTTGACCAACTCCAGTTGTTAAAGTCACTCAT 1380
QY 1381 GTGACTGCACTGAAATCTAAGGATCGGAAAGAAATCTGTGGTTCCAGGAGAAATTCCTTT 1440
DB 1381 GTGACTGCACTGAAATCTAAGGATCGGAAAGAAATCTGTGGTTCCAGGAGAAATTCCTTT 1440
QY 1441 TCAGAAATCAGCCATTTCTCTCTTAAGATGGTTTTAGAGTCTTTGCCAGAAAGATGA 1500
DB 1441 TCAGAAATCAGCCATTTCTCTCTTAAGATGGTTTTAGAGTCTTTGCCAGAAAGATGA 1500
QY 1501 GGGTTTAACTGAAATTAAGATGATCTGCCAGAAAGGATGGAATGCGGATGGTAAC 1560
DB 1501 GGGTTTAACTGAAATTAAGATGATCTGCCAGAAAGGATGGAATGCGGATGGTAAC 1560
QY 1561 TTATCAACATATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAACTGTTTGTAGAA 1620
DB 1561 TTATCAACATATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAACTGTTTGTAGAA 1620
QY 1621 AATTTCTGGGAGGAGGAATAGTGTCTTCTTCAATTTGATGCAGATATTTGCACAAATGTT 1680
DB 1621 AATTTCTGGGAGGAGGAATAGTGTCTTCTTCAATTTGATGCAGATATTTGCACAAATGTT 1680
QY 1681 CGGCAAAAGCAGAAACAAATATCCGATACTATTTTAACTCAAGAAAAATCTGAGATTTAT 1740
DB 1681 CGGCAAAAGCAGAAACAAATATCCGATACTATTTTAACTCAAGAAAAATCTGAGATTTAT 1740
QY 1741 CCTGAACTCATGGACCTCAGATCTCGGACAAACCCCAATTCGAGCTTTGACAGTTT 1800
DB 1741 CCTGAACTCATGGACCTCAGATCTCGGACAAACCCCAATTCGAGCTTTGACAGTTT 1800
QY 1801 GAAATCTACTGGGGAATAATGTATACATCTGAAGACTTGTCTCAGAAAAACCCATCTATATT 1860
DB 1801 GAAATCTACTGGGGAATAATGTATACATCTGAAGACTTGTCTCAGAAAAACCCATCTATATT 1860

1801 GAAATCTACTGGGTAATAATGTACATACTGAAGACTTCTCAGAAACCCATCCTATATT 1860
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1861 CAAGAGCAAAAGCTAAGGAGCTAGTCATATTCTCTGCTGGGGTGATGATACCAATGATCCT 1920
1921 GAAAACAGAGGAAATGAAGGAACTTGAGTTAATGGTCTAATTTATGATAGGATATAT 1980
1921 GAAAACAGAGGAAATGAAGGAACTTGAGTTAATGGTCTAATTTATGATAGGATATAT 1980
1981 GATTGATGCTGCAACAAACCAATATATTCGAAGTGGAGCAATTCGAAGCCCTGAGCAG 2040
1981 GATTGATGCTGCAACAAACCAATATATTCGAAGTGGAGCAATTCGAAGCCCTGAGCAG 2040
2041 GAATGCCAGAGCTTAAGAGCTGTTTGTGTCCTCAGCTTTAGCGCTTTGTCCTCATCT 2100
2041 GAATGCCAGAGCTTAAGAGCTGTTTGTGTCCTCAGCTTTAGCGCTTTGTCCTCATCT 2100
2101 TTGTGGGGAGTCTGATATCCATGATGGATGCCAAGCAATGATAAATGAGGAATGCT 2160
2101 TTGTGGGGAGTCTGATATCCATGATGGATGCCAAGCAATGATAAATGAGGAATGCT 2160
2161 TAGTTTTTATTCACAGAGCTCAATTTGGGGGGTGCACCGCTGTTCTGGGTATTCATTT 2220
2161 TAGTTTTTATTCACAGAGCTCAATTTGGGGGGTGCACCGCTGTTCTGGGTATTCATTT 2220
2221 TTTCATCAGTGAAGCTGTTGATCTATGCTTTTGGGCTTCTCAGTTCATGAAGCAATAA 2280
2221 TTTCATCAGTGAAGCTGTTGATCTATGCTTTTGGGCTTCTCAGTTCATGAAGCAATAA 2280
2281 TGAAGTATTTAACTCTTTCACAGTCTTTCAGAGTATGCTATTTAAATTAATCTTGGCCA 2340
2281 TGAAGTATTTAACTCTTTCACAGTCTTTCAGAGTATGCTATTTAAATTAATCTTGGCCA 2340
2341 GGTATAATTCAGCTCAGTCTCTTTATAGTGAGAAAAATTTATGTTAGTAGTATAATAA 2400
2341 GGTATAATTCAGCTCAGTCTCTTTATAGTGAGAAAAATTTATGTTAGTAGTATAATAA 2400
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2401 TTTTAACTAAATATATAATCTATAATCTTAAACATATGTTTCATTTAAAGCATAGCACT 2460
2461 TTGAAATTAATATATAATAGCTCATATTTACACTACAGCTTTTCATTTGATCAGGTC 2520
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2521 TGAATCTTTAGCACTTAAGGAAATGACTATGCTATGCTAATTTACCTGACCATGAAAAA 2580
2521 TGAATCTTTAGCACTTAAGGAAATGACTATGCTAATTTACCTGACCATGAAAAA 2580
2581 TAAGTACCTCAATGATCATCTTTGACCTGGTGTTCACCACTGCAAAATCTTTTGCCA 2640
2581 TAAGTACCTCAATGATCATCTTTGACCTGGTGTTCACCACTGCAAAATCTTTTGCCA 2640
2641 TCTTGATATAGGATATTTTATCATGGGTGATGATGACATGACACCAACCACTTTTCATTCAGT 2700
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2701 ATGAACCTTGAGGCTGCTGCCATTTTTCATTAACCAACCAAGCTGAAGGTGAACCTC 2760
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2761 GAACTGTTTTCATTAATCTTTTCAAAAGTGTGTTTACATCAATGTTTAAATTTCAAAATG 2820
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2821 CTGAGGGTAAATTTATGATATAAATATTTAGTAAAGAAAAAGTATGTTATGTCATCTAGT 2880
2821 CTGAGGGTAAATTTATGATATAAATATTTAGTAAAGAAAAAGTATGTTATGTCATCTAGT 2880
2881 AGAATAGATCAACAATCAAAATTCATTTCACTGATGCTTTAGTGTGTTAAAGCATGAGAT 2940

2881 AGAATAGATCAACAATCAAAATTCATTTCACTGATGCTTTAGTGTGTTAAAGCATGAGAT 2940
2941 TGTACATGTTTACTGTTAGGTCCTTTGCACTCTGTGCTAGTGTAGTATGAGAAATGTC 3000
2941 TGTACATGTTTACTGTTAGGTCCTTTGCACTCTGTGCTAGTGTAGTATGAGAAATGTC 3000
3001 AAGGACTGGAGTATTTGTTGCTTAAATAAAAAAGGCTGTTTGTAGGCGTTTAAATAT 3060
3001 AAGGACTGGAGTATTTGTTGCTTAAATAAAAAAGGCTGTTTGTAGGCGTTTAAATAT 3060
3061 GCTTATTTTGTGTCCTCTCACTACTATACACTGTTGCTTTGTCGGTGTGTTTGT 3120
3061 GCTTATTTTGTGTCCTCTCACTACTATACACTGTTGCTTTGTCGGTGTGTTTGT 3120
3121 ATGTCGCTGTGTTATACACTAGTATTAATTTCCATGACAGAAAAATAATGTCGTAATCT 3180
3121 ATGTCGCTGTGTTATACACTAGTATTAATTTCCATGACAGAAAAATAATGTCGTAATCT 3180
3181 CAAAAAATAAAAAAAGGCGCGCGC 3206
3181 CAAAAAATAAAAAAAGGCGCGCGC 3206

RESULT 2
ABS56723
ID ABS56723 standard; cDNA; 3206 BP.
XX
AC ABS56723;
XX
DT 24-FEB-2003 (first entry)
XX
DE Human NARC16 cDNA.
XX
KW NARC16; NARC16; cytostatic; immunosuppressive; dermatological; cardiac;
antiinflammatory; nephrotropic; anti-HIV; nontropic; neuroprotective;
antianemic; cerebroprotective; vasotropic; antidiabetic; anticonvulsant;
immunosuppressive; thymimetic; immunostimulant; antianemic; hypotensive;
tranquilliser; neuroleptic; gene therapy; gene mapping; apoptosis;
AIDS; cell cycle disruption; programmed cell death regulation;
viral infection; nucleosome assembly; follicular lymphoma; carcinoma;
cell cycle regulation; cancer; follicular lymphoma; carcinoma;
p53 mutation; graft rejection; hormone-dependent tumour;
autoimmune disorder; valvular heart disease;
systemic lupus erythematosus; diabetes; Hashimoto's thyroiditis;
immune-mediated glomerulonephritis; virus-induced lymphocyte depletion;
acquired immunodeficiency syndrome; neurodegenerative disease; stroke;
Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
spinal muscular atrophy; retinitis pigmentosa; myocardial infarction;
myelodysplastic syndrome; ischaemic injury; myocardial infarction;
reperfusion injury; liver disease; idiopathic dilated cardiomyopathy;
ischaemic cardiomyopathy; aplastic anaemia; chronic neutropenia; mania;
myelodysplastic syndrome; central nervous system disorder; anxiety;
senile dementia; Huntington's disease; hypertension; schizophrenia;
severe bipolar affective disorder; human; chromosome 4q11-4q21; ss.

Homo sapiens.
OS
XX
FH Key Location/Qualifiers
CDS 145..2163
FT /*tag= a
FT /product= "NARC16"
XX
PN WO200281516-A2.
XX
PD 17-OCT-2002.
XX
PF 16-JAN-2002; 2002WO-US001098.
XX
PR 16-JAN-2001; 2001US-0262306P.
XX
PR 15-JAN-2002; 2002US-00047855.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX

PI Chiang LW;
DR WPI; 2003-058503/05.
DR P-ESDB; ABB84606.
XX Novel isolated programmed cell death-related polypeptide, NARC10 and
PT NARC16, useful for treating disorders associated with abnormal apoptotic
PT process e.g. Alzheimer's disease, cancer, myocardial infarction, stroke.
XX Claim 1; Fig 4A-C; 123pp; English.
XX This invention describes novel cell death-related polypeptides NARC10 and
XX NARC16, located on chromosome 4q11-4q21 and which have cardiant, antiHIV,
XX immunosuppressive, dermatological, antiinflammatory, cerebroprotective,
XX neotropic, neuroprotective, antianemic, cardiant, vasotropic, antianemic,
XX antidiabetic, immunosuppressive, cytostatic; hyprometric, nephrotropic,
XX immunostimulant, anticonvulsant, tranquiliser, hypertensive and
XX neuroleptic activity and can be used in gene therapy. The products of the
XX invention can be used to modulate NARC10 or NARC16 polypeptides or
XX polynucleotides, to map NARC genes on a chromosome, e.g. to locate gene
XX regions associated with genetic disease or to associate NARC10 or NARC16
XX with a disease. The polypeptides are also useful for modulating the
XX apoptotic process, and are therefore useful for modulating, and treating
XX disorders associated with increased apoptosis, inhibition of apoptosis or
XX disruptions in cell cycle, for regulating cellular functions including
XX programmed cell death, nucleosome assembly, phosphate homeostasis and the
XX cell cycle. Preferably, the products of the invention are useful for
XX treating disorders associated with abnormally low rate or abnormally high
XX rate of apoptosis e.g. cancers including follicular lymphomas, carcinomas
XX with p53 mutations, or hormone-dependent tumours, autoimmune disorders
XX including systemic lupus erythematosus, diabetes, graft rejection,
XX Hashimoto's thyroiditis and immune-mediated glomerulonephritis and viral
XX infections e.g. infections caused by herpes viruses, virus-induced
XX lymphocyte depletion (including acquired immunodeficiency syndrome
XX (AIDS)), neurodegenerative diseases manifested by loss of specific sets
XX of neurons (including Alzheimer's disease, Parkinson's disease,
XX amyotrophic lateral sclerosis, spinal muscular atrophy, retinitis
XX pigmentosa, and cerebellar degeneration), myelodysplastic syndromes
XX (including aplastic anaemia), ischaemic injuries (including myocardial
XX infarction, stroke and reperfusion injury), and toxin (e.g. alcohol)
XX induced liver disease, idiopathic dilated cardiomyopathy, ischaemic
XX cardiomyopathy and valvular heart disease, aplastic anaemia, chronic
XX neutropenia, and myelodysplastic syndromes, central nervous system
XX disorders, senile dementia, Huntington's disease, hypertension,
XX schizophrenia, attention deficit disorder, mania, anxiety, severe bipolar
XX affective disorder (BP-I). This sequence encodes the human NARC16 protein
XX described in the method of the invention
SQ Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;
Query Match 100.0%; Score 3206; DB 8; Length 3206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCCACGGCTCGGGCGAGGACGACGAGCGGGGCGCGGTAACCTCTGCCCGCGGT 60
DB 1 GTGACCCACGGCTCGGGCGAGGACGACGAGCGGGGCGCGGTAACCTCTGCCCGCGGT 60
QY 61 CCTCGCTCTCGGGCGGGGCGGGCGACCGGACCTGCGGACTAGCGAACCCGGAGCAG 120
DB 61 CCTCGCTCTCGGGCGGGGCGGGCGACCGGACCTGCGGACTAGCGAACCCGGAGCAG 120
QY 121 ACATCAATAAAATCAATCAGATGACACCTTCTCAGGTGGCTTTTGAAATAAGAGGA 180
DB 121 ACATCAATAAAATCAATCAGATGACACCTTCTCAGGTGGCTTTTGAAATAAGAGGA 180
QY 181 ACTCTTTTACCAGAGGAAGTTTTCGATATGTGGAAGCTGTGATCTTTGGGAACCTGG 240
DB 181 ACTCTTTTACCAGAGGAAGTTTTCGATATGTGGAAGCTGTGATCTTTGGGAACCTGG 240
QY 241 AATCCTCAAAATCTGTGGCTCTCTTCCAGAGAATGACACAGGTGAAGCATGCTATGG 300
DB 241 AATCCTCAAAATCTGTGGCTCTCTTCCAGAGAATGACACAGGTGAAGCATGCTATGG 300

QY 301 AAAGCAACCATTTGTACTCAGTAGAGGAGTATCAGTTCAGTATCGCTACTTCAAGGGTAC 360
DB 301 AAAGCAACCATTTGTACTCAGTAGAGGAGTATCAGTTCAGTATCGCTACTTCAAGGGTAC 360
QY 361 TTTTGTAGAACCAAGACTATCGGTGGTCCATGTCAGTCAAGTGAAGTATCAAGTGGGAGACT 420
DB 361 TTTTGTAGAACCAAGACTATCGGTGGTCCATGTCAGTCAAGTGAAGTATCAAGTGGGAGACT 420
QY 421 CATCTACCAACCAAGTCAATTAACCCCTTTAGAAAGCGAAATTTATTATTGACGATGACAA 480
DB 421 CATCTACCAACCAAGTCAATTAACCCCTTTAGAAAGCGAAATTTATTATTGACGATGACAA 480
QY 481 TTTGGAATCCCAATAGGTGTTGAAACTCTGGATTCTGGATGCTGACATGTCAGATGAA 540
DB 481 TTTGGAATCCCAATAGGTGTTGAAACTCTGGATTCTGGATGCTGACATGTCAGATGAA 540
QY 541 ATAAGATTACGTTTGATTTCTGAAACACCTCTGTCTCAATTAACCAAGAAAAAATTA 600
DB 541 ATAAGATTACGTTTGATTTCTGAAACACCTCTGTCTCAATTAACCAAGAAAAAATTA 600
QY 601 AAAAAATCTAGATTTAGGTGAGCTGACACTAGAGGCTCGAGGAAGATGACGATGAT 660
DB 601 AAAAAATCTAGATTTAGGTGAGCTGACACTAGAGGCTCGAGGAAGATGACGATGAT 660
QY 661 AGGTATCTCCCACTGTACTTCCACAAAAATGTCCAATAGCTTTGGAGATATCTTTAAGC 720
DB 661 AGGTATCTCCCACTGTACTTCCACAAAAATGTCCAATAGCTTTGGAGATATCTTTAAGC 720
QY 721 GACAATGAGTTCAAGTGCAGGCAATTCACAGCGGAGTGGTTATGGCTTGCAGCCTGAT 780
DB 721 GACAATGAGTTCAAGTGCAGGCAATTCACAGCGGAGTGGTTATGGCTTGCAGCCTGAT 780
QY 781 CGTTGACAGAGTACAGCATACAGAGTGGACAGATTAACCTGGAATCTTATCTTTGAT 840
DB 781 CGTTGACAGAGTACAGCATACAGAGTGGACAGATTAACCTGGAATCTTATCTTTGAT 840
QY 841 TTTTTCGAGAAGATCTCAGTGAGCAGTAGTTTCAGGCTGATGCCCTTCTCTGACATGTG 900
DB 841 TTTTTCGAGAAGATCTCAGTGAGCAGTAGTTTCAGGCTGATGCCCTTCTCTGACATGTG 900
QY 901 GGTACAGCTTGTCTTATCATCCATTCCTGCTGAGAGTGGAAAGAGTGTGGAATCTT 960
DB 901 GGTACAGCTTGTCTTATCATCCATTCCTGCTGAGAGTGGAAAGAGTGTGGAATCTT 960
QY 961 ACTCTTCCCATCATGACAGCAAAATCCCGGAAACCAATAGGCAAGTGGAGTTGACTAT 1020
DB 961 ACTCTTCCCATCATGACAGCAAAATCCCGGAAACCAATAGGCAAGTGGAGTTGACTAT 1020
QY 1021 ATAATTATTAAAGCCATTACCAGGATACAGTTGTGACATGAAATCTTCTTCCAAAGTAT 1080
DB 1021 ATAATTATTAAAGCCATTACCAGGATACAGTTGTGACATGAAATCTTCTTCCAAAGTAT 1080
QY 1081 TGAAGCCAAAGAAATACCATTTGGGATTTGGCCATCGAGGTGACGAAACTCTCAACAAC 1140
DB 1081 TGAAGCCAAAGAAATACCATTTGGGATTTGGCCATCGAGGTGACGAAACTCTCAACAAC 1140
QY 1141 GCCCAGCTGGCTAAAGTTCAAGAAAATACATTTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
DB 1141 GCCCAGCTGGCTAAAGTTCAAGAAAATACATTTGCTTCTTTAAGAAATGCTGCTAGTCAT 1200
QY 1201 GGTGACGCTTTGTAGAAATTTGAGTACACCTTTCAAGAGGACTTTGTGCCCGCTGGTATAT 1260
DB 1201 GGTGACGCTTTGTAGAAATTTGAGTACACCTTTCAAGAGGACTTTGTGCCCGCTGGTATAT 1260
QY 1261 CATGATCTTACCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTA 1320
DB 1261 CATGATCTTACCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTA 1320
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DB 1321 TTTGAAATTCAGTAAAGAAATTAACATTTGACCACTCCAGTTGTTTAAAGCTCAGTCAT 1380

QY 1381 GTGACTGCACTGAAATCTAAGGATCGAAGAAATCTGTGGTTCAGGAGGAAATTCCTTT 1440
Db 1381 GTGACTGCACTGAAATCTAAGGATCGAAGAAATCTGTGGTTCAGGAGGAAATTCCTTT 1440
QY 1441 TCAGAAAATCAGCCATTCCTCTCTTAAAGATGGTTTAAAGTCTTTGCGCAGAAAGATGA 1500
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QY 1501 GGGTTTAAACATTTGAAATTAATAATCGATCTGCGCAGAAAAGGATGGAATTTGGATGGTAAC 1560
Db 1501 GGGTTTAAACATTTGAAATTAATAATCGATCTGCGCAGAAAAGGATGGAATTTGGATGGTAAC 1560
QY 1561 TTATCAACATATTTTTCACATGAATCTGTTTGGATATAATTTTAAAGAACTGTCTTTAGAA 1620
Db 1561 TTATCAACATATTTTTCACATGAATCTGTTTGGATATAATTTTAAAGAACTGTCTTTAGAA 1620
QY 1621 AATTTCTGGGAAGAGGAGATAGTGTCTTCTTCAATTTGATGCGAGATATTTTGCACAATGGTT 1680
Db 1621 AATTTCTGGGAAGAGGAGATAGTGTCTTCTTCAATTTGATGCGAGATATTTTGCACAATGGTT 1680
QY 1681 CGGCAAAAGCAGAACAAATATCCGATATCTATTTTAACTCAAGGAAATCTGAGATTTAT 1740
Db 1681 CGGCAAAAGCAGAACAAATATCCGATATCTATTTTAACTCAAGGAAATCTGAGATTTAT 1740
QY 1741 CCTGAATCATGCACTCAGATCTCGGACACCCCAATTCGATGAGCTTTGCAAGATTT 1800
Db 1741 CCTGAATCATGCACTCAGATCTCGGACACCCCAATTCGATGAGCTTTGCAAGATTT 1800
QY 1801 GAAATCTACTGGGGAATTAATGATACATCTGGAAGACTCTGAGAACCCATCTATATT 1860
Db 1801 GAAATCTACTGGGGAATTAATGATACATCTGGAAGACTCTGAGAACCCATCTATATT 1860
QY 1861 CAAGAGCAAAAGCTAAGGAGCTAGTCAATTTCTGCTGGGGTGATGATACCAATGATCT 1920
Db 1861 CAAGAGCAAAAGCTAAGGAGCTAGTCAATTTCTGCTGGGGTGATGATACCAATGATCT 1920
QY 1921 GAAACAGAGGAAATTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACT 1980
Db 1921 GAAACAGAGGAAATTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAACT 1980
QY 1981 GATTGATGCTTGAACCAATATATTCAGAGTGAAGCAATTCGAGCGCTGAGAGAG 2040
Db 1981 GATTGATGCTTGAACCAATATATTCAGAGTGAAGCAATTCGAGCGCTGAGAGAG 2040
QY 2041 GAATTCAGAGCTTAAAGAGCTGTTTGTGCTCCACTGTTAGCGCTTTGTTCCCTCATCT 2100
Db 2041 GAATTCAGAGCTTAAAGAGCTGTTTGTGCTCCACTGTTAGCGCTTTGTTCCCTCATCT 2100
QY 2101 TTGTGTGGGGAGTCTGATATCCATGTTGATGATGATGATGATGATGATGATGATGATGAT 2160
Db 2101 TTGTGTGGGGAGTCTGATATCCATGTTGATGATGATGATGATGATGATGATGATGATGAT 2160
QY 2161 TAGTTTATTCACAGAGTCAATTTTGGGGGCTGACCGCTGTTCTGGGTATTCATTT 2220
Db 2161 TAGTTTATTCACAGAGTCAATTTTGGGGGCTGACCGCTGTTCTGGGTATTCATTT 2220
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Db 2221 TTCACTCAGTGAATTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAA 2280
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Db 2281 TGAAGTATTTAACTCTTTTCACTACAGTCTTTCGAAAGTATGCTATTTAAATTTACTTGGCA 2340
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QY 2521 TGAAATCTTTTAGCACTTAAAGGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 2521 TGAAATCTTTTAGCACTTAAAGGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
QY 2581 TAAGTACCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
Db 2581 TAAGTACCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2640
QY 2641 TCTTGTATATAGGTATTTTACATGCGTGGTGGATGATGATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 TCTTGTATATAGGTATTTTACATGCGTGGTGGATGATGATGATGATGATGATGATGATGATGATGAT 2700
QY 2701 ATGAACCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
Db 2701 ATGAACCTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2760
QY 2761 GAAACTTCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCT 2820
Db 2761 GAAACTTCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCTTTTCAATAATCT 2820
QY 2821 CTGAGGGTAAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
Db 2821 CTGAGGGTAAATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2880
QY 2881 AGAATAGATCAACAATCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAAT 2940
Db 2881 AGAATAGATCAACAATCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAATTTCAAT 2940
QY 2941 TGTACATGTTTACTGTTAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
Db 2941 TGTACATGTTTACTGTTAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3000
QY 3001 AAGGACTGGAGCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
Db 3001 AAGGACTGGAGCTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3060
QY 3061 GCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
Db 3061 GCTTATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120
QY 3121 ATGTCGCTGCTTATACAGTATGTTTAAATTTTCCATGAGGAAATTAATTTCTGCTGCTGCTGCTGCT 3180
Db 3121 ATGTCGCTGCTTATACAGTATGTTTAAATTTTCCATGAGGAAATTAATTTCTGCTGCTGCTGCTGCT 3180
QY 3181 CAAAAAAGGAGGCGCGC 3206
Db 3181 CAAAAAAGGAGGCGCGC 3206
RESULT 3
ADJ57933
ID ADJ57933 standard; cDNA; 3206 BP.
XX
AC ADJ57933;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human NARC 16B cDNA.
XX
KW Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
KW lung disease; cirrhosis; hepatitis; atherosclerosis;
KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;
KW drug screening; gene therapy; cytostatic; hepatotropic; neurotropic;
KW cerebrotective; dermatological; viricide; neuroprotective;
XX phosphatidylglycerol phosphate synthase; PGP synthase; human; ss.
XX Homo sapiens.
OS

US2004009553-A1.
15-JAN-2004.
30-APR-2003; 2003US-00426776.
27-SEP-1999; 99US-00406045.
22-OCT-1999; 99US-0161188P.
31-JAN-2000; 2000US-00495823.
28-FEB-2000; 2000US-0185517P.
20-OCT-2000; 2000US-00692785.
31-JAN-2001; 2001US-00773426.
28-FEB-2001; 2001US-00795691.
31-OCT-2001; 2001US-0335003P.
31-OCT-2001; 2001US-0335037P.
25-MAR-2002; 2002US-00105992.
28-AUG-2002; 2002US-00229662.
30-OCT-2002; 2002US-00284014.
30-OCT-2002; 2002US-00284059.
09-DEC-2002; 2002US-00314881.
(MILL-) MILLENNIUM PHARM INC.
Glucksmann MA, Williamson MJ, Tsai F, Rudolph-Owen LA;
Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
WPI; 2004-090469/09.
New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 22438, 23553, NARC SCL or NARC 1) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer, atherosclerosis or AIDS.
Claim 1; SEQ ID NO 34; 260pp; English.
The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SCL, NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or 32222. The invention is useful in diagnosing, preventing or treating disorders such as cancer, lung diseases, cirrhosis, hepatitis, atherosclerosis, myocardial infarction, inflammation, anaemia, glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency syndrome), Parkinson's disease, Alzheimer's disease, stroke and dermatitis. These may also be used in drug screening. The invention is also useful in gene therapy. The present sequence is human neuronal apoptosis regulated candidate (NARC) cDNA.
Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;
Query Match 100.0%; Score 3206; DB 12; Length 3206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGACCCACGGCTCGGGCGAGGACGCGACGGCGGGCGCCGGTACCTCTGCCCGCGGT 60
DB 1 GTCGACCCACGGCTCGGGCGAGGACGCGACGGCGGGCGCCGGTACCTCTGCCCGCGGT 60
QY 61 CCTCGCTCTCGGGCGGGCGGGCGGACGCGGACCTGCGGACTAGCGAACCCGGAGACG 120
DB 61 CCTCGCTCTCGGGCGGGCGGGCGGACGCGGACCTGCGGACTAGCGAACCCGGAGACG 120
QY 121 ACATCATATAAATCCATCAGATGACACCTTCTCAGGTTGCCTTTGAAATAGAGGA 180
DB 121 ACATCATATAAATCCATCAGATGACACCTTCTCAGGTTGCCTTTGAAATAGAGGA 180
QY 181 ACTCTTTTACAGGAGAGTCTTTTGGATATGTGGAAGCTGTGATGCTTTGGGAACTGG 240
DB 181 ACTCTTTTACAGGAGAGTCTTTTGGATATGTGGAAGCTGTGATGCTTTGGGAACTGG 240
QY 241 AATCCTCAAAATGCTGTGGCTCTTCTTCCAGAGAATGACACAGGTGAAGCATGCTATGG 300

DB 241 AATCCTCAAAATGCTGTGGCTCTTCTTCCAGAGAATGACACAGGTGAAGCATGCTATGG 300
QY 301 AAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 360
DB 301 AAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 360
QY 361 TTTTAAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 420
DB 361 TTTTAAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 420
QY 421 CATCTACAAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 480
DB 421 CATCTACAAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 480
QY 481 TTTTAAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 540
DB 481 TTTTAAAGCAACCATTTGTAAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 540
QY 541 ATAAGATTAGTTTGAAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 600
DB 541 ATAAGATTAGTTTGAAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 600
QY 601 AAAAAATCTAGATTAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 660
DB 601 AAAAAATCTAGATTAGGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 660
QY 661 AGGGTATCTCCACTGATCTTCAAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 720
DB 661 AGGGTATCTCCACTGATCTTCAAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 720
QY 721 GACAAATGAGTTCAAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 780
DB 721 GACAAATGAGTTCAAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 780
QY 781 CGTTGGACAGATGATCAGGATGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 840
DB 781 CGTTGGACAGATGATCAGGATGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 840
QY 841 TTTTTCGAAGAAGATCTCAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 900
DB 841 TTTTTCGAAGAAGATCTCAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 900
QY 901 GGTACAGTTGCTCTTATCATCCATTCAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 960
DB 901 GGTACAGTTGCTCTTATCATCCATTCAGTTCGAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 960
QY 961 ACTCTTCCCATCATGAGCAGAAATTCGCGGAAACCAATAGGCAAGTTCGAGTTCGCTACTTCAAGGGTAC 1020
DB 961 ACTCTTCCCATCATGAGCAGAAATTCGCGGAAACCAATAGGCAAGTTCGAGTTCGCTACTTCAAGGGTAC 1020
QY 1021 ATAATTATTAAGCCATTCAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1080
DB 1021 ATAATTATTAAGCCATTCAGGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1080
QY 1081 TGGAGCAAGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1140
DB 1081 TGGAGCAAGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1140
QY 1141 GCCCAGCTGGCTAAAGTTCAAGAAATATCTATTCCTTTTAAAGAAATGCTGCTAGTTCAT 1200
DB 1141 GCCCAGCTGGCTAAAGTTCAAGAAATATCTATTCCTTTTAAAGAAATGCTGCTAGTTCAT 1200
QY 1201 GGTGAGCCTTTTGAAGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1260
DB 1201 GGTGAGCCTTTTGAAGATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1260
QY 1261 CATGATCTTACCTGTTTGAATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1320
DB 1261 CATGATCTTACCTGTTTGAATGATCAGTTTCAAGTTCGCTACTTCAAGGGTAC 1320
QY 1321 TTTTCAAAATCCAGTAAAGAAATTAACATTTGACCACTCCAGTTGTTTAAAGCTCACTCAT 1380
DB 1321 TTTTCAAAATCCAGTAAAGAAATTAACATTTGACCACTCCAGTTGTTTAAAGCTCACTCAT 1380

XX 21-MAR-2000; 2000US-0191031P.
PR 25-MAY-2000; 2000US-0207124P.
PR 15-JUN-2000; 2000US-0211940P.
PR 07-JUL-2000; 2000US-0216820P.
PR 25-JUL-2000; 2000US-0220661P.
PR 21-DEC-2000; 2000US-0257672P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Lee J, Lillie J;
XX WPI; 2001-611502/70.
XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX
XX Disclosure: SEQ ID NO 21000; 106pp; English.
XX
XX The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the
CC invention.
XX
SQ Sequence 3499 BP; 1104 A; 610 C; 736 G; 1039 T; 0 U; 10 Other;
Query Match 98.8%; Score 3166; DB 5; Length 3499;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 11 GCCTCGGGGAGGCGACGACGCGGGCGCGCGGTACCTCTGCCGCGGTCTCGCTCTC 70
DB 87 GAGCGCTGGCGAGGACGACGCGGGCGCGCGGTACCTCTGCCGCGGTCTCGCTCTC 146
QY 71 GGGCGGGGCGGGCGGACCGGACCTGCGGACCTAGCGAACCCGAGCAGCATCATAA 130
DB 147 GGGCGGGGCGGGCGGACCGGACCTGCGGACCTAGCGAACCCGAGCAGCATCATAA 206
QY 131 ATAAATCCATCAGAATGACACCTTCTCAGGTGCGCTTTGAAATPAAGAGAACTCTTTTAC 190
DB 207 ATAAATCCATCAGATGACACCTTCTCAGGTGCGCTTTGAAATPAAGAGAACTCTTTTAC 266
QY 191 CAGGAGAGGTTTTTGGGATATGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAA 250
DB 267 CAGGAGAGGTTTTTGGGATATGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAA 326

QY 251 ATGCTGTGGCTCTTCTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAGCAACCA 310
DB 327 ATGCTGTGGCTCTTCTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAGCAACCA 386
QY 311 TTGTACTCAGTAGAGAGGATATCAGTTTCAGTATCGCTACTTTCAAAGGGTACTTTTGAAC 370
DB 387 TTGTACTCAGTAGAGAGGATATCAGTTTCAGTATCGCTACTTTCAAAGGGTACTTTTGAAC 446
QY 371 CAAAGACTATCGGTGGTCCATGTCAGTGATGATTTTCAAGTGGGAGACTCATCTACAC 430
DB 447 CAAAGACTATCGGTGGTCCATGTCAGTGATGATTTTCAAGTGGGAGACTCATCTACAC 506
QY 431 CAGGATCAATAAACCCTTTAGAAAAGCGAAATTTATTGACCATGGAACAATTTGGAATCC 490
DB 507 CAGGATCAATAAACCCTTTAGAAAAGCGAAATTTATTGACCATGGAACAATTTGGAATCC 566
QY 491 ACAATGGTGTGAAACTCTCTGGATTTCTGGATGGCTGACATGTGAGACTGAAATAAGATTAC 550
DB 567 ACAATGGTGTGAAACTCTCTGGATTTCTGGATGGCTGACATGTGAGACTGAAATAAGATTAC 626
QY 551 GTTTGCATTATTCTGAAAACCTCTGTGTCAATTAACCAAGAAAATAATTAATAATCTTA 610
DB 627 GTTTGCATTATTCTGAAAACCTCTGTGTCAATTAACCAAGAAAATAATTAATAATCTTA 686
QY 611 GATTAGGTGAGCTGACACATAGAGGCTCTGAGGAAGATGACATGATAGGTATCTC 670
DB 687 GATTAGGTGAGCTGACACATAGAGGCTCTGAGGAAGATGACATGATAGGTATCTC 746
QY 671 CCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTTAATPAAGCGACAATGAGT 730
DB 747 CCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTTAATPAAGCGACAATGAGT 806
QY 731 TCAAGTCGAGGCAATCACAGCCGAGTGTGTATGGCTTGAGCCCTGATCTGTGGACAG 790
DB 807 TCAAGTCGAGGCAATCACAGCCGAGTGTGTATGGCTTGAGCCCTGATCTGTGGACAG 866
QY 791 AGTACAGCATACAGAGATGGAACCAAGTAACTGGAACCTAATCTTTTGAATTTTTCGAAG 850
DB 867 AGTACAGCATACAGAGATGGAACCAAGTAACTGGAACCTAATCTTTTGAATTTTTCGAAG 926
QY 851 AAGATCTCAGTGAGCAGCTAGTTTCAGGGTGATGCCCTTCTTGACATGTGGGTACAGCTT 910
DB 927 AAGATCTCAGTGAGCAGCTAGTTTCAGGGTGATGCCCTTCTTGACATGTGGGTACAGCTT 986
QY 911 GTCTTTATCATCCACATTTGCTGAGAGTGGAAAGAGTGTCTGAAATCTTACTCTTCCCA 970
DB 987 GTCTTTATCATCCACATTTGCTGAGAGTGGAAAGAGTGTCTGAAATCTTACTCTTCCCA 1046
QY 971 TCATGACAGAAATTCGCCGAAAACCAATAGGAAAGTGAAGTGTGACTATATAATTTA 1030
DB 1047 TCATGACAGAAATTCGCCGAAAACCAATAGGAAAGTGAAGTGTGACTATATAATTTA 1106
QY 1031 AGCCATTACAGGATACAGTTGTGACATGAAATCTTTCATTTTCCAGATTTGGAAGCCAA 1090
DB 1107 AGCCATTACAGGATACAGTTGTGACATGAAATCTTTCATTTTCCAGATTTGGAAGCCAA 1166
QY 1091 GAATACCATTTGGATTTGGCCATCGAGTGCAGGAAACTCTCAACAACTGCCAGCTGG 1150
DB 1167 GAATACCATTTGGATTTGGCCATCGAGTGCAGGAAACTCTCAACAACTGCCAGCTGG 1226
QY 1151 CTAAGTTCAAGAAAATACTATTGCTTTTAAAGAAATGCTGTAGTTCATGGTGCAGCT 1210
DB 1227 CTAAGTTCAAGAAAATACTATTGCTTTTAAAGAAATGCTGTAGTTCATGGTGCAGCT 1286
QY 1211 TTGTAGAAATTTGAGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTA 1270
DB 1287 TTGTAGAAATTTGAGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTA 1346
QY 1271 CCTGTGTTTGAATGATAAGAAAATAATTTGATGCTGATGCTGAAATTTTGAATTC 1330
DB 1347 CCTGTGTTTGAATGATAAGAAAATAATTTGATGCTGATGCTGAAATTTTGAATTC 1406

QY	1331	CAGTAAAGAAATTAACATTTGACCAACTCCAGTGTGTTAAAGCTCACTCATGTGACGTGCAC	1390
Db	1407	CAGTAAAGAAATTAACATTTGACCAACTCCAGTGTGTTAAAGCTCACTCATGTGACGTGCAC	1466
QY	1391	TGAAATCTAAGGATCGGAAGAAATCTGTGTTCCAGCAGGAAATCTCTTTTCAGAAATC	1450
Db	1467	TGAAATCTAAGGATCGGAAGAAATCTGTGTTCCAGCAGGAAATCTCTTTTCAGAAATC	1526
QY	1451	AGCCATTTCTCTTCTTAAGATGGTTTCTTAAGTCTTTGCGCAGAGATGTAGGGTTTAAACA	1510
Db	1527	AGCCATTTCTCTTCTTAAGATGGTTTCTTAAGTCTTTGCGCAGAGATGTAGGGTTTAAACA	1586
QY	1511	TTGAAATAAATGGATCTGCCAGCAAAAGGATGGAATGTGGGATGTAACTATCAACAT	1570
Db	1587	TTGAAATAAATGGATCTGCCAGCAAAAGGATGGAATGTGGGATGTAACTATCAACAT	1646
QY	1571	ATTTTCACATGAATCTGTTTCTTGATATAATTTTAAAGCTGTTTAAAGAAATCTGGCA	1630
Db	1647	ATTTTCACATGAATCTGTTTCTTGATATAATTTTAAAGCTGTTTAAAGAAATCTGGCA	1706
QY	1631	AGAGGAGAATAGTGTGTTTCTTCAATTTGATGCGAGATATTTGCACAATGGTTCGGCAAAAGC	1690
Db	1707	AGAGGAGAATAGTGTGTTTCTTCAATTTGATGCGAGATATTTGCACAATGGTTCGGCAAAAGC	1766
QY	1691	AGAACAAAATATCCGATACATATTTTAACTCAAGGAAATCTGAGATTTATCCTGAACTCA	1750
Db	1767	AGAACAAAATATCCGATACATATTTTAACTCAAGGAAATCTGAGATTTATCCTGAACTCA	1826
QY	1751	TGGACCTCAGATCTCGGCAACCCCAATTCGCAATGAGCTTGCACAGTTTGAATCTAC	1810
Db	1827	TGGACCTCAGATCTCGGCAACCCCAATTCGCAATGAGCTTGCACAGTTTGAATCTAC	1886
QY	1811	TGGGATAAATGTACATCTGAAGACTGTCTCAGAAACCCATCTCTATATTTCAAGAGGCAA	1870
Db	1887	TGGGATAAATGTACATCTGAAGACTGTCTCAGAAACCCATCTCTATATTTCAAGAGGCAA	1946
QY	1871	AGCTAAGGACTAGTCTATATCTGCTGGGGTGAATGATACCAATGATCTGAAACAGAA	1930
Db	1947	AGCTAAGGACTAGTCTATATCTGCTGGGGTGAATGATACCAATGATCTGAAACAGAA	2006
QY	1931	GGAAATGAAGAACTGTGAGTAAATGCTTAATTTATGATAGGATATGATGATGTC	1990
Db	2007	GGAAATGAAGAACTGTGAGTAAATGCTTAATTTATGATAGGATATGATGATGTC	2066
QY	1991	CTGAACAAACCAATATATTTCCAGTGGAGCAATTTGGAACCCCTGAGCAGGAATTCGCCAG	2050
Db	2067	CTGAACAAACCAATATATTTCCAGTGGAGCAATTTGGAACCCCTGAGCAGGAATTCGCCAG	2126
QY	2051	AGCTTAAGAGCTGTTGTGTCACATCTGTTAGCGCTTGTGTTCCCTCATCTTTGTGGGG	2110
Db	2127	AGCTTAAGAGCTGTTGTGTCACATCTGTTAGCGCTTGTGTTCCCTCATCTTTGTGGGG	2186
QY	2111	AGTCTGATATCCATGTGGATGCGCAACCGCATTTGATACGTGGAGATGCTTAGTTTAT	2170
Db	2187	AGTCTGATATCCATGTGGATGCGCAACCGCATTTGATACGTGGAGATGCTTAGTTTAT	2246
QY	2171	TGCACAGAGCTCATTTTGGGGGGTGCACCGCTGTTCTGGGTATTCATTTTTCATCACTG	2230
Db	2247	TGCACAGAGCTCATTTTGGGGGGTGCACCGCTGTTCTGGGTATTCATTTTTCATCACTG	2306
QY	2231	AGCATTTGATATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATTAATGAAGTATTT	2290
Db	2307	AGCATTTGATATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATTAATGAAGTATTT	2366
QY	2291	AACTCTTTCACATCAGTCTTGCAGATGCTATTTTAAATTAATCTTGGCCAGGATTAATTTG	2350
Db	2367	AACTCTTTCACATCAGTCTTGCAGATGCTATTTTAAATTAATCTTGGCCAGGATTAATTTG	2426
QY	2351	CCAGTCAGTCTCTTTTATAGTGAAGAAATTTTATTTGGTTAGTAAATATTTTAAACTA	2410
Db	2427	CCAGTCAGTCTCTTTTATAGTGAAGAAATTTTATTTGGTTAGTAAATATTTTAAACTA	2486
QY	2411	AATATATAAATCTATATGTTTAAACATATGTTTCAATTTAAAGCATAGCACTTTGAAATTA	2470

RESULT 5

ADN05171

ID ADN05171 standard; cDNA; 5443 BP.

XX AC ADN05171;

XX AC ADN05171;

DT 01-JUL-2004 (first entry)

XX AC ADN05171;

DE Antipsoriatic cDNA sequence #801.

XX AC ADN05171;

KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.

XX AC ADN05171;

OS Homo sapiens.

XX AC ADN05171;

PN WO2004028479-A2.

XX AC ADN05171;

PD 08-APR-2004.

XX AC ADN05171;

PF 25-SEP-2003; 2003WO-US030907.

XX AC ADN05171;

PR 25-SEP-2002; 2002US-0414006P.

XX AC ADN05171;

XX	(GETH) GENENTECH INC.
XX	Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX	Wu TD;
PI	XX
PI	XX
DR	WPI; 2004-305105/28.
DR	P-PSDB; ADN05172.
XX	New PRO nucleic acid or polypeptide, useful for preparing a
PT	pharmaceutical composition for diagnosing or treating psoriasis in a
PT	mammal.
XX	Claim 1; SEQ ID NO 1565; 3069pp; English.
PS	XX
PS	XX
CC	The invention relates to novel polynucleotide and polypeptides for
CC	treating psoriasis or a sequence having at least 80% identity to the
CC	above sequences. The nucleic acid is useful for preparing a composition
CC	for diagnosing or treating psoriasis in a mammal. This sequence
CC	corresponds to one of the polynucleotides of the invention.
XX	Sequence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;
SQ	
	Query Match 98.8%; Score 3166; DB 12; Length 5443;
	Best Local Similarity 99.8%; Pred. No. 0;
	Matches 3169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy	11 GCCTCGGGCGGACGAGCAGCGGGGGGCCCGGTACTCTGCCCCGGGTCTCGCTTC 70
Dd	71 GAGCGCTGGCGAGCGACGAGCGGGCGGCCCGGTACTCTGCCCCGGGTCTCGCTTC 130
Qy	71 GGGCGGGCGCGCGACGCGCGAAGCTGCGGAAGTGCAGAACCCGAGACGACATCAAAA 130
Dd	131 GGGCGGGCGCGCGACGCGCGAAGCTGCGGAAGTGCAGAACCCGAGACGACATCAAAA 190
Qy	131 ATAAATCATCAGATGACACCTTCTCAGGTGCTTTGAATAAGAGGAAGTCTTTTAC 190
Dd	191 ATAAATCATCAGATGACACCTTCTCAGGTGCTTTGAATAAGAGGAAGTCTTTTAC 250
Qy	191 CAGGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTGGGAACTGGAAATCCTCAA 250
Dd	251 CAGGAGAAGTTTTTGCGATATGTGGAAGCTGTGATGCTTTGGGAACTGGAAATCCTCAA 310
Qy	251 ATGCTGTGGCTCTTCTCCAGAGATGACACAGGTGAAAGCATGCTATGGAAGCAACA 310
Dd	311 ATGCTGTGGCTCTTCTCCAGAGATGACACAGGTGAAAGCATGCTATGGAAGCAACA 370
Qy	311 TTGTAAGTAGAGGAGTATCAGTTTCAGTATCGCTACTTCAAGGGTACTTTTTAGAAC 370
Dd	371 TTGTAAGTAGAGGAGTATCAGTTTCAGTATCGCTACTTCAAGGGTACTTTTTAGAAC 430
Qy	371 CAAGACTATCGGTGCTCCATGCTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC 430
Dd	431 CAAGACTATCGGTGCTCCATGCTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC 490
Qy	431 CACGATCAATAACCCCTTTAGAAAGCGAAATTATTATTGACGATGGACAATTTGGAATCC 490
Dd	491 CACGATCAATAACCCCTTTAGAAAGCGAAATTATTATTGACGATGGACAATTTGGAATCC 550
Qy	491 ACAATGGTGTGAAACTCTGGATTTCTGGATGCTGACATGTCAGACTGNAATTAAGTTAC 550
Dd	551 ACAATGGTGTGAAACTCTGGATTTCTGGATGCTGACATGTCAGACTGNAATTAAGTTAC 610
Qy	551 GTTTCGATTTCTGAAAAACCTCTGCTCAATAACCAAGAAAAAATTTAAAAAATCTTA 610
Dd	611 GTTTCGATTTCTGAAAAACCTCTGCTCAATAACCAAGAAAAAATTTAAAAAATCTTA 670
Qy	611 GATTTAGGTGAAGCTGACACTAGAGGCTCGAGGAAGATGACGATGATGGGTATCTTC 670
Dd	671 GATTTAGGTGAAGCTGACACTAGAGGCTCGAGGAAGATGACGATGATGGGTATCTTC 730
Qy	671 CCACCTGTACTCCAATAATGTCCAATAGCTTTGGAGATATCTTTAATAACGCAATGAGT 730

Db	731	CCACGTGTA	CTCCACAAATGTCC	CAATAGCTTGGAGATAC	CTTAAATAGCGCAATGAGT	790
Qy	731	TCAGTGCAGGCAT	TTCACAGCGGAGTGTG	GTATATGGCTTGAGCCTGAT	TCGTTGCAGCAG	790
Db	791	TCAGTGCAGGCAT	TTCACAGCGGAGTGTG	GTATATGGCTTGAGCCTGAT	TCGTTGCAGCAG	850
Qy	791	AGTACAGCATACAG	ACGATGGAACACAGATA	TAACCTCGAACTAATCT	TGATTTTTTCGAG	850
Db	851	AGTACAGCATACAG	ACGATGGAACACAGATA	TAACCTCGAACTAATCT	TGATTTTTTCGAG	910
Qy	851	AGATCTCAGTCAG	CAGCAGCTAGTTC	CAGGGTGATGCCCTT	CCTCGACAATGTGGGTACAGCTT	910
Db	911	AGATCTCAGTCAG	CAGCAGCTAGTTC	CAGGGTGATGCCCTT	CCTCGACAATGTGGGTACAGCTT	970
Qy	911	GTCTCTTATCAT	CTCCACATTCGTG	AGAGTGGAAAGAGTCT	CGAAATCTTACTCTTCCCA	970
Db	971	GTCTCTTATCAT	CTCCACATTCGTG	AGAGTGGAAAGAGTCT	CGAAATCTTACTCTTCCCA	1030
Qy	971	TCATGACGAGAAAT	TCCCGGAAAAA	CAATAGGCAAAAGTGAGAGT	TGACTATATAATTTATTA	1030
Db	1031	TCATGACGAGAAAT	TCCCGGAAAAA	CAATAGGCAAAAGTGAGAGT	TGACTATATAATTTATTA	1090
Qy	1031	AGCCATTAC	CCAGGATACAGTGTG	CACTGAAATCTTCA	TTTTCCAAAGTATGGAAAGCCAA	1090
Db	1091	AGCCATTAC	CCAGGATACAGTGTG	CACTGAAATCTTCA	TTTTCCAAAGTATGGAAAGCCAA	1150
Qy	1091	GAATACCAT	TGGATGTGGCCAT	CGAGGTGCAGGAAATCT	CAACAACTGCCAGCTGG	1150
Db	1151	GAATACCAT	TGGATGTGGCCAT	CGAGGTGCAGGAAATCT	CAACAACTGCCAGCTGG	1210
Qy	1151	CTAAAGTTC	CAAGAAATACATAT	TGCTTTTAAAGAAATGCTG	CTAGTCACTGGTGCAGCCT	1210
Db	1211	CTAAAGTTC	CAAGAAATACATAT	TGCTTTTAAAGAAATGCTG	CTAGTCACTGGTGCAGCCT	1270
Qy	1211	TTGTAGAA	TTTGCAGTACACCTTT	CAAGAGACTTTG	TGCGGAGTATCATGATCTTA	1270
Db	1271	TTGTAGAA	TTTGCAGTACACCTTT	CAAGAGACTTTG	TGCGGAGTATCATGATCTTA	1330
Qy	1271	CCTGTTGTTT	GACTATGAAAAA	GAATTTGATGCTGAT	CCAGTTGGAATTAATTTGAAATTC	1330
Db	1331	CCTGTTGTTT	GACTATGAAAAA	GAATTTGATGCTGAT	CCAGTTGGAATTAATTTGAAATTC	1390
Qy	1331	CAGTAAAGAA	TTAAACATTTGACCA	ATCTCAGTTGTTTAAAGCT	CACCTCATGTGACATGCAC	1390
Db	1391	CAGTAAAGAA	TTAAACATTTGACCA	ATCTCAGTTGTTTAAAGCT	CACCTCATGTGACATGCAC	1450
Qy	1391	TGAAATCTAAG	GTACGGAAGATCTG	TGCTTCAGGAGGAAATTC	CTTTTCAGAAAAATC	1450
Db	1451	TGAAATCTAAG	GTACGGAAGATCTG	TGCTTCAGGAGGAAATTC	CTTTTCAGAAAAATC	1510
Qy	1451	AGCATTTCTCT	CTTTAAGATGGTTT	TAGAGTCTTTGCCAGAGATGT	TAGGGTTTAAACA	1510
Db	1511	AGCATTTCTCT	CTTTAAGATGGTTT	TAGAGTCTTTGCCAGAGATGT	TAGGGTTTAAACA	1570
Qy	1511	TTGAAATAA	AAATGGATCTGCCACAA	AGGATGGAATGTGGGATG	TGTAACCTTATCAACAT	1570
Db	1571	TTGAAATAA	AAATGGATCTGCCACAA	AGGATGGAATGTGGGATG	TGTAACCTTATCAACAT	1630
Qy	1571	ATTTTGATCA	TGAATCTGTTTTTGGATA	TAAATTTTAAAACTGTTTT	TAGAAAAATCTCGGGA	1630
Db	1631	ATTTTGATCA	TGAATCTGTTTTTGGATA	TAAATTTTAAAACTGTTTT	TAGAAAAATCTCGGGA	1690
Qy	1631	AGAGGAA	TAGTGTCTTTCTTCA	TTTTGATGCAGATATTTGCACA	ATGGTTTCGCAAAAAGC	1690
Db	1691	AGAGGAA	TAGTGTCTTTCTTCA	TTTTGATGCAGATATTTGCACA	ATGGTTTCGCAAAAAGC	1750
Qy	1691	AGAACAA	ATATCCGATACTATTTT	TAACTCAAGGAAATCTGAGAT	TTATCCTGAACTCA	1750
Db	1751	AGAACAA	ATATCCGATACTATTTT	TAACTCAAGGAAATCTGAGAT	TTATCCTGAACTCA	1810
Qy	1751	TGGACCT	CAGATCTCGACACACCC	CAATGCCAATGAGCTTTG	CACAGTTTGAATAATCTAC	1810
Db	1811	TGGACCT	CAGATCTCGACACACCC	CAATGCCAATGAGCTTTG	CACAGTTTGAATAATCTAC	1870

1811 TGGGGATAAATGTACATCTGAAGACTTGTCTCAGAAACCCATCCTATATTCGAAGGGCAA 1870
1871 TGGGGATAAATGTACATCTGAAGACTTGTCTCAGAAACCCATCCTATATTCGAAGGGCAA 1930
1871 AAGCTAAGGGACTAGTCATATTCCTGCTGGGGTGATGATACCAATGATCCTGAACAGAA 1930
1931 AAGCTAAGGGACTAGTCATATTCCTGCTGGGGTGATGATACCAATGATCCTGAACAGAA 1990
1931 GGAATTGAAGGAACCTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATGATGC 1990
1991 GGAATTGAAGGAACCTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATGATGC 2050
1991 CTGAACAACCAATATATTCGAAGTGAGCAATTTGAAGCGCTGAGAGCAAGTAATGCCAG 2050
2051 CTGAACAACCAATATATTCGAAGTGAGCAATTTGAAGCGCTGAGAGCAAGTAATGCCAG 2110
2051 AGCTTAAGAGCTGTTTGTGCTCCCACTGTTAGCGCTTGTTCCTCATCTTTGTGCGGG 2110
2111 AGCTTAAGAGCTGTTTGTGCTCCCACTGTTAGCGCTTGTTCCTCATCTTTGTGCGGG 2170
2111 AGCTGATATCCATGTGATGTCACCGCATTTGATAACCTGGAGATGCTTAGTTTTTAT 2170
2171 AGCTGATATCCATGTGATGTCACCGCATTTGATAACCTGGAGATGCTTAGTTTTTAT 2230
2171 TGCACAGAGGTCAATTTTGGGGCGTGCACCGCTGTTCTGGGTATTCAATTTTCACTACTG 2230
2231 TGCACAGAGGTCAATTTTGGGGCGTGCACCGCTGTTCTGGGTATTCAATTTTCACTACTG 2290
2231 AGCATTTGTATCTATGCCCTTTTGGCTTCTCAGTTCAATGAAGCAATTAATGAATATT 2290
2291 AGCATTTGTATCTATGCCCTTTTGGCTTCTCAGTTCAATGAAGCAATTAATGAATATT 2350
2291 AACTCTTTTCACTACAGTTCTTCAAGTATGCTATTTAAATTAATCTGGCCAGGTATAATG 2350
2351 AACTCTTTTCACTACAGTTCTTCAAGTATGCTATTTAAATTAATCTGGCCAGGTATAATG 2410
2351 CCAGTCAGTCTCTTTATAGTGAGAAATTTATTTGGTTAGTAAATATAAATTTTAAACTA 2410
2411 CCAGTCAGTCTCTTTATAGTGAGAAATTTATTTGGTTAGTAAATATAAATTTTAAACTA 2470
2411 AATATATAATCTATAATGTTTAAACATATGTTTCATTAAGCATAGCACCTTTGAAATTA 2470
2471 AATATATAATCTATAATGTTTAAACATATGTTTCATTAAGCATAGCACCTTTGAAATTA 2530
2471 CTATATAATAGTCTCATATTTACATTTACAGTCTTTTCAATTCAGTCTCAAAATCTTT 2530
2531 CTATATAATAGTCTCATATTTACATTTACAGTCTTTTCAATTCAGTCTCAAAATCTTT 2590
2531 AGCATTGAAGGAAATGACTATGCTATAATTTATACCTGACCATGAAACCAATTAAGTACCTC 2590
2591 AGCATTGAAGGAAATGACTATGCTATAATTTATACCTGACCATGAAACCAATTAAGTACCTC 2650
2591 AATGATGATGATGCTGCTGATGCTCAATTCGACCAATCTTTGTGCAATCTTGTATAT 2650
2651 AATGATGATGATGCTGCTGATGCTCAATTCGACCAATCTTTGTGCAATCTTGTATAT 2710
2651 AGGTATTTTACATGGGTTGATGCTGACACCAACCAATTTTCAATTCAGTATGAACCTTG 2710
2711 AGGTATTTTACATGGGTTGATGCTGACACCAACCAATTTTCAATTCAGTATGAACCTTG 2770
2711 AGGCTGCTGCCATTTTCCACTTAACCAACCGAGCTGAAAGTGAACCTTGGT 2770
2771 AGGCTGCTGCCATTTTCCACTTAACCAACCGAGCTGAAAGTGAACCTTGGT 2830
2771 TCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGCGGGTA 2830
2831 TCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGCGGGTA 2890
2831 ATTTAATGATATAAATATTTAGTAAAGAAAGTATGTTGATGCTACTTAGTAAATAGATC 2890
2891 ATTTAATGATATAAATATTTAGTAAAGAAAGTATGTTGATGCTACTTAGTAAATAGATC 2950

2891 ACAACATACAAATTCATTCAGTGCATGCTTTAGTGTAAAGCATGAGATTGTACATGTT 2950
2951 ACAACATACAAATTCATTCAGTGCATGCTTTAGTGTAAAGCATGAGATTGTACATGTT 3010
2951 TACTGTTAGGTCCTTGCATCTGTGCTGCTAGTGTAGTATGAGAAGCATGCAAGGACTGGA 3010
3011 TACTGTTAGGTCCTTGCATCTGTGCTGCTAGTGTAGTATGAGAAGCATGCAAGGACTGGA 3070
3011 CGTATTTTGTGCTTAAACCAAGGCTGTTTGTAGCGCTTTTAAATATGCTTATTTTG 3070
3071 CGTATTTTGTGCTTAAACCAAGGCTGTTTGTAGCGCTTTTAAATATGCTTATTTTG 3130
3071 TGTGCTCTCACTACCTATTAACACCTGCTTGTGCTTGTGCGGTTTGTGATGTCGCTGT 3130
3131 TGTGCTCTCACTACCTATTAACACCTGCTTGTGCTTGTGCGGTTTGTGATGTCGCTGT 3190
3131 GTTATACAGTAGTTAAATTTCCATGCAGAAAATAAATGCTCTGAATTTCTCAA 3184
3191 GTTATACAGTAGTTAAATTTCCATGCAGAAAATAAATGCTCTGAATTTCTCAT 3244

RESULT 6
ADS74320
ID ADS74320 standard; cDNA; 5443 BP.
XX
AC ADS74320;
XX AC
XX DT 16-DEC-2004 (first entry)
XX
DE PRO83903 cDNA clone DNA327983, role in immune-related disease.
XX
KW PRO83903; Crohn's disease; rheumatoid arthritis; gastrointestinal-gen.;
XX antirheumatic; antiarthritic; psoriasis; antipsoriatic; gene; ss.
XX Homo sapiens.
FH Key Location/Qualifiers
FT CDS 190..2223
FT /*tag= a
FT /product= "PRO83903"
FT /partial
FT /note= "No start codon"
XX
PN WO2004081199-A2.
XX
XX 23-SEP-2004.
XX
XX 10-MAR-2004; 2004WO-US007862.
XX
XX 11-MAR-2003; 2003US-0454025P.
XX (GETH) GENENTECH INC.
XX
XX Baldwin D, Bodary S, Clark H, Pong S, Gurney AL, Williams PM;
XX
XX WPI; 2004-668955/65.
XX P-PSDB; ADS74321.
XX
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
XX treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
XX arthritis.
XX
XX Claim 1; SEQ ID NO 39; 166pp; English.
XX
XX The present sequence is of cDNA clone DNA327983 encoding novel human PRO
XX polypeptide. PRO83903. The invention provides newly identified and
XX isolated nucleotide sequences encoding polypeptides referred to as PRO
XX polypeptides that are useful in the diagnosis and treatment of immune-
XX related diseases. Microarray analysis showed that DNA327983 is up-
XX regulated 1.5-fold in lesional skin as compared to non-lesional skin from
XX psoriasis patients, up-regulated 1.3-fold in colon samples from Crohn's
XX disease patients as compared to normal colon and up-regulated 1.3-fold in
XX white blood cells from rheumatoid arthritis patients as compared to those

CC from healthy donors. It is also down-regulated 1.5-fold upon activation
CC of CD4 T cells with CD28 or ICAM and down-regulated 2-fold upon
CC activation of monocytes with LPS. PR083903 can be used in a claimed
CC method of identifying a compound that inhibits expression of the gene
CC encoding it. The candidate compound is especially an antisense nucleic
CC acid. The PRO polypeptide, its antagonist or an antibody that binds the
CC polypeptide are used in claimed methods for the alleviation or diagnosis
CC of rheumatoid arthritis, Crohn's disease and psoriasis. A vector
CC comprising the present nucleic acid can be used to transform a host cell,
CC especially a CHO cell, Escherichia coli or yeast, for production of the
CC PRO polypeptide.
XX

Sequence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;

Query Match 98.8%; Score 3166; DB 13; Length 5443;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3169; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	11	CGCTCCGGGCGGACGCGAGCGGGGCGCCGGTACCTCTGCGCGGGTCTCGCTCTC	70
Db	71	GAGCGCTGGCGAGGACGCGAGCGGGGCGCCGGTACCTCTGCGCGGGTCTCGCTCTC	130
Qy	71	GGGCGGGCGGGCGGACGCGGACTCGGACTAGCGAACCGGAGCACGACATCAAAA	130
Db	131	GGGCGGGCGGGCGGACGCGGACTCGGACTAGCGAACCGGAGCACGACATCAAAA	190
Qy	131	ATAAATCCATCAGATGACACCTCTCAGGTTGCTTTGAAATAGAGGAACTCTTTTAC	190
Db	191	ATAAATCCATCAGATGACACCTCTCAGGTTGCTTTGAAATAGAGGAACTCTTTTAC	250
Qy	191	CAGGAGAGTTTTTCGATATGTGAAGCTGTGATGCTTTTGGGAACTGGAACTCTCAA	250
Db	251	CAGGAGAGTTTTTCGATATGTGAAGCTGTGATGCTTTTGGGAACTGGAACTCTCAA	310
Qy	251	ATGCTGTGCTCTCTTCCAGAGATGACAGGTTGAAGCATGCTATGGAAGCAACCA	310
Db	311	ATGCTGTGCTCTCTTCCAGAGATGACAGGTTGAAGCATGCTATGGAAGCAACCA	370
Qy	311	TTGTACTCAGTAGAGGATGATCAGTTTCTGCTACTCTCAAGGGTACTTTTTAGAAC	370
Db	371	TTGTACTCAGTAGAGGATGATCAGTTTCTGCTACTCTCAAGGGTACTTTTTAGAAC	430
Qy	371	CAAAGACTATCGGTGGTCCATGTCAGTATGATAGTTTCAAGTGGGAGATCTATCAAC	430
Db	431	CAAAGACTATCGGTGGTCCATGTCAGTATGATAGTTTCAAGTGGGAGATCTATCAAC	490
Qy	431	CAGCATCAATTAACCCCTTTAGAAAGCAATTTATTTGACCATGACAAATTTGGAATCC	490
Db	491	CAGCATCAATTAACCCCTTTAGAAAGCAATTTATTTGACCATGACAAATTTGGAATCC	550
Qy	491	ACAATGGTGTGAACTCTGGATTTCTGGATGGTGCATGTCAGACTGAAATTAAGTTAC	550
Db	551	ACAATGGTGTGAACTCTGGATTTCTGGATGGTGCATGTCAGACTGAAATTAAGTTAC	610
Qy	551	GTTTGGCATTTTCTGAAAACTCTCTGTGTCAATAACCAAGAAAAATTTAAAAAATCTA	610
Db	611	GTTTGGCATTTTCTGAAAACTCTCTGTGTCAATAACCAAGAAAAATTTAAAAAATCTA	670
Qy	611	GATTTAGGGTGAAGCTGACACTAGAGGCTGGAGGAGATGCGATGATAGGGTATCTC	670
Db	671	GATTTAGGGTGAAGCTGACACTAGAGGCTGGAGGAGATGCGATGATAGGGTATCTC	730
Qy	671	CCACTGTACTCCAAAAATGTCAAATAGCTTGGAGATATCTTTAATAAGCGACAATGAGT	730
Db	731	CCACTGTACTCCAAAAATGTCAAATAGCTTGGAGATATCTTTAATAAGCGACAATGAGT	790
Qy	731	TCAAGTGCAGGCAATTCACAGCCGGAGTGGTGTATAGCTTGCAGCTGATCGTTGGACAG	790
Db	791	TCAAGTGCAGGCAATTCACAGCCGGAGTGGTGTATAGCTTGCAGCTGATCGTTGGACAG	850
Qy	791	AGTACAGCATACAGACGATGGAACCACTGGAATCTAATCTTTGATTTTTTCGAAG	850
Db	851	AGTACAGCATACAGACGATGGAACCACTGGAATCTAATCTTTGATTTTTTCGAAG	910

Qy	851	AAGATCTCAGTGAGCAGCAGTAGTTGAGGTGATGCCCTTCTGGACATGTGGGTACAGCTT	910
Db	911	AAGATCTCAGTGAGCAGCAGTAGTTGAGGTGATGCCCTTCTGGACATGTGGGTACAGCTT	970
Qy	911	GTCTCTTATCATCCACCATGCTGAGAGTGAAAGAGTGTGGAATCTTACTCTTCCCA	970
Db	971	GTCTCTTATCATCCACCATGCTGAGAGTGAAAGAGTGTGGAATCTTACTCTTCCCA	1030
Qy	971	TATGAGCAGAAATTTCCGGAACCAATAGCAAGTGTGAGTGTGACTATATAATTATTA	1030
Db	1031	TATGAGCAGAAATTTCCGGAACCAATAGCAAGTGTGAGTGTGACTATATAATTATTA	1090
Qy	1031	AGCCATTACAGGATACAGTTGTCGATGAAATCTTTTCCAAAGTATTGGAGCCAA	1090
Db	1091	AGCCATTACAGGATACAGTTGTCGATGAAATCTTTTCCAAAGTATTGGAGCCAA	1150
Qy	1091	GAATACCATTTGGATGTGGCCATCGAGGTGCAGGAACTCTTACCAACTGCCAGCTGG	1150
Db	1151	GAATACCATTTGGATGTGGCCATCGAGGTGCAGGAACTCTTACCAACTGCCAGCTGG	1210
Qy	1151	CTAAAGTTCAGAAAAATCTATTGCTTCTTAAAGAAATGCTCTAGTCAATGTCAGCT	1210
Db	1211	CTAAAGTTCAGAAAAATCTATTGCTTCTTAAAGAAATGCTCTAGTCAATGTCAGCT	1270
Qy	1211	TTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGTATATCATCTTA	1270
Db	1271	TTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGTATATCATCTTA	1330
Qy	1271	CTGTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTC	1330
Db	1331	CTGTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTC	1390
Qy	1331	CAGTAAAGAAATTAACATTTGACCACTCAGTTGTTAAAGCTCACTCATGTGCTGAC	1390
Db	1391	CAGTAAAGAAATTAACATTTGACCACTCAGTTGTTAAAGCTCACTCATGTGCTGAC	1450
Qy	1391	TGAAATCTAAGGATCGGAAAGAAATCTGTGTTTCAAGAGGAAATTTCTTTTCAAGAAATC	1450
Db	1451	TGAAATCTAAGGATCGGAAAGAAATCTGTGTTTCAAGAGGAAATTTCTTTTCAAGAAATC	1510
Qy	1451	AGCCATTTCTTCTCTTAAAGATGTTTGAAGTCTTTTGCAGAGATGTAGGGTTTAAAC	1510
Db	1511	AGCCATTTCTTCTCTTAAAGATGTTTGAAGTCTTTTGCAGAGATGTAGGGTTTAAAC	1570
Qy	1511	TTGAAATAAATCGATCTGCCAGCAAGGATGGAATGTGGGATGTAACTTATCAACAT	1570
Db	1571	TTGAAATAAATCGATCTGCCAGCAAGGATGGAATGTGGGATGTAACTTATCAACAT	1630
Qy	1571	ATTTTGCATGAATCTGTTTTTGGATATAATTTTAAACCTGTTTTAGAAAAATCTGGGA	1630
Db	1631	ATTTTGCATGAATCTGTTTTTGGATATAATTTTAAACCTGTTTTAGAAAAATCTGGGA	1690
Qy	1631	AGAGGAAATAGTGTGTTTTCTTCAATTTGATGCAATTTTGCACAAATGGTTCGGCAAAAGC	1690
Db	1691	AGAGGAAATAGTGTGTTTTCTTCAATTTGATGCAATTTTGCACAAATGGTTCGGCAAAAGC	1750
Qy	1691	AGAAACAAATATCCGATCTATTTTAACTCAAGGAAATCTGAGATTTTCTTGAATCTCA	1750
Db	1751	AGAAACAAATATCCGATCTATTTTAACTCAAGGAAATCTGAGATTTTCTTGAATCTCA	1810
Qy	1751	TGGACCTCAGATCTCGGACCAACCCCATTCGAATGAGCTTTTGACAGATTTTGAATCTAC	1810
Db	1811	TGGACCTCAGATCTCGGACCAACCCCATTCGAATGAGCTTTTGACAGATTTTGAATCTAC	1870
Qy	1811	TGGGGTAAATGTACATCTGAAGATGCTGAGAAACCCCATTCCTATTTTCAAGAGGCAA	1870
Db	1871	TGGGGTAAATGTACATCTGAAGATGCTGAGAAACCCCATTCCTATTTTCAAGAGGCAA	1930
Qy	1871	AAGCTAAGGGACTAGTCTATTTCTGCTGGGGTGTATACCAATGATCTCTGAAACAGAA	1930
Db	1931	AAGCTAAGGGACTAGTCTATTTCTGCTGGGGTGTATACCAATGATCTCTGAAACAGAA	1990

Qy	1931	GGAAATTGAAGCAACTTGGAGTTAAATGGTCTAAATTTATGATAGCATATATGATTTGAAATGC	1991
Db	1991	GGAAATTGAAGCAACTTGGAGTTAAATGGTCTAAATTTATGATAGCATATATGATTTGAAATGC	2050
Qy	1991	CTGAACCAACCAAAATATATTTCCAAGTGGAGCAATTTGGAACGCCTCAAGCAGGAATTCGCAG	2050
Db	2051	CTGAACCAACCAAAATATATTTCCAAGTGGAGCAATTTGGAACGCCTCAAGCAGGAATTCGCAG	2110
Qy	2051	AGCTTAAAGAGCTGTTTGTGTCGCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2110
Db	2111	AGCTTAAAGAGCTGTTTGTGTCGCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2170
Qy	2111	AGTCTGATATCCATGTGATGCCCAACCGCATTTGATTAACGTGGAGAAATGCTTAGTTTTTAT	2170
Db	2171	AGTCTGATATCCATGTGATGCCCAACCGCATTTGATTAACGTGGAGAAATGCTTAGTTTTTAT	2230
Qy	2171	TGCACAGAGGTCATTTTGGGGGCGTGACCGCTGTTCTGGGTATTCATTTTTCATCACTG	2230
Db	2231	TGCACAGAGGTCATTTTGGGGGCGTGACCGCTGTTCTGGGTATTCATTTTTCATCACTG	2290
Qy	2231	AGCAATTGTTGATCTATGCTTTTGGGCTTCTCAGTTCCAATGAAGCAATAATGAAGTATTT	2290
Db	2291	AGCAATTGTTGATCTATGCTTTTGGGCTTCTCAGTTCCAATGAAGCAATAATGAAGTATTT	2350
Qy	2291	AATCTTTTCACTACAGTCTTTGCAAGTATGCTATTTAAATTTACCTGCGCCAGGTAAATG	2350
Db	2351	AATCTTTTCACTACAGTCTTTGCAAGTATGCTATTTAAATTTACCTGCGCCAGGTAAATG	2410
Qy	2351	CCAGTCAGTCTCTTTATAGTGGAGAAATTTATTTGGTTAGTAAATAATAATTTTAACTA	2410
Db	2411	CCAGTCAGTCTCTTTATAGTGGAGAAATTTATTTGGTTAGTAAATAATAATTTTAACTA	2470
Qy	2411	AAATATAAAATCTATAATGTTTAAACATATGTTTCATTAAGCAATAGCACCTTTGAAATTA	2470
Db	2471	AAATATAAAATCTATAATGTTTAAACATATGTTTCATTAAGCAATAGCACCTTTGAAATTA	2530
Qy	2471	CTATATAAAATAGCTCATATTTTACACTTACAGCTTTTTCATTGTGATCAGGTCGAAATCTTT	2530
Db	2531	CTATATAAAATAGCTCATATTTTACACTTACAGCTTTTTCATTGTGATCAGGTCGAAATCTTT	2590
Qy	2531	AGCACTTAAAGGAAATGACATATGCATAATTTATACCTGACCATGAAAAAATAAGTACCTC	2590
Db	2591	AGCACTTAAAGGAAATGACATATGCATAATTTATACCTGACCATGAAAAAATAAGTACCTC	2650
Qy	2591	AAATGCATGCATTTGCACTGGTGATTCCAACTGCAACAAATCTTTGTGCCATCTTGATAT	2650
Db	2651	AAATGCATGCATTTGCACTGGTGATTCCAACTGCAACAAATCTTTGTGCCATCTTGATAT	2710
Qy	2651	AGGTATTTTTTACATGGGTTGACATGCACACAACACCATTTTTCATTGATGAAACCTTG	2710
Db	2711	AGGTATTTTTTACATGGGTTGACATGCACACAACACCATTTTTCATTGATGAAACCTTG	2770
Qy	2711	AGGCTGCTGCCATTTTCCACTTAAACCAACCGCTGGAAGGTGAACCTCGAAACTTGTT	2770
Db	2771	AGGCTGCTGCCATTTTCCACTTAAACCAACCGCTGGAAGGTGAACCTCGAAACTTGTT	2830
Qy	2771	TCATAAATCTTTCAAAGATGTTTTCATCAATGTTTAAATTTCAAATGCTCGAGGTA	2830
Db	2831	TCATAAATCTTTCAAAGATGTTTTCATCAATGTTTAAATTTCAAATGCTCGAGGTA	2890
Qy	2831	ATTTAAATGTTATAAAATATTAGTAAGAAAAAGTATGTTAGTCATCTTTAGTAGAATAGATC	2890
Db	2891	ATTTAAATGTTATAAAATATTAGTAAGAAAAAGTATGTTAGTCATCTTTAGTAGAATAGATC	2950
Qy	2891	ACAACATACAAATTCAAATTCAGTGCATGCTTTTAGTGTGTTAAGCATGAGATGTGACATGTT	2950
Db	2951	ACAACATACAAATTCAAATTCAGTGCATGCTTTTAGTGTGTTAAGCATGAGATGTGACATGTT	3010
Qy	2951	TACTGTTTAGGTCTTGTGCATCTGTGTGCTAGGTGAGTATGAGAAGATGTCACAGCATGGA	3010
Db	3011	TACTGTTTAGGTCTTGTGCATCTGTGTGCTAGGTGAGTATGAGAAGATGTCACAGCATGGA	3070
Qy	3011	CGTATTTTGTGCTTAAAAAAGGCTGTTTGTAGGCGCTTTTAAATATGCTTATTTTGTG	3070

Db	3071	CGTATTTTGTGGCTTAAATAAAGGCTGTTTGTAGCGCTTTTAAATATGCTTATTTG	3130
Qy	3071	TGTGTCTCTCACTACCTATTACACACATGTTTGCCTTTTGGGCTTTTGTATGTGGCTGT	3130
Db	3131	TGTGTCTCTCACTACCTATTACACACATGTTTGTGGGCTTTTGTATGTGGCTGT	3190
Qy	3131	GTTATACAGTAGTAAATTTCCATGCAGAAAAATAAATATGCTGAATCTCAA	3184
Db	3191	GTTATACAGTAGTAAATTTCCATGCAGAAAAATAAATGTCCTGAATCTCATA	3244
RESULT 7			
ABV29614			
XX	ID	ABV29614 standard; cDNA; 3499 BP.	
XX	AC	ABV29614;	
XX	DT	16-SEP-2002 (first entry)	
XX	DE	Human prostate expression marker cDNA 29605.	
XX	KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;	
XX	KW	pharmacogenomic marker; gene; ss.	
XX	OS	Homo sapiens.	
XX	XX	WO200160860-A2.	
XX	XX	23-AUG-2001.	
XX	PD		
XX	PF	20-FEB-2001; 2001WO-US005171.	
XX	PR	17-FEB-2000; 2000US-0183319P.	
XX	PR	16-MAR-2000; 2000US-0189862P.	
XX	PR	25-MAY-2000; 2000US-0207454P.	
XX	PR	09-JUN-2000; 2000US-0211314P.	
XX	PR	18-JUL-2000; 2000US-0219007P.	
XX	PR	13-DEC-2000; 2000US-0255281P.	
XX	PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	PI	Schlegel R, Endege WO, Monahan JE;	
XX	PI	WPI; 2001-662795/76.	
XX	DR		
XX	PT	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.	
XX	PT	Claim 1; Page 6349; 11750pp; English.	
XX	PS		
XX	XX	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker	
XX	XX	Sequence 3499 BP; 1104 A; 609 C; 736 G; 1040 T; 0 U; 10 Other;	
SQ			
Query Match			
Best Local Similarity 98.7%; Score 3164.4; DB 5; Length 3499;			
Matches 3168; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
Qy	11	CGGTCCGGGCGAGCGACGACGGCGGCGCCCGGTACCTCTGCCCGGCTCTCGCTTC	70

Db 87 GAGCGCTGGCAGGSCAGGACGGCGGGCGCCGGTACCTCTGCCGCGGTCTCGCTCTC 146
Qy 71 GGGCGGGCGCGCGAGCGCGA CCTCGGAGCTAGCGAA CCGGAGCAGCAGCATATAA 130
Db 147 GGGCGGGCGCGCGAGCGCGA CCTCGGAGCTAGCGAA CCGGAGCAGCAGCATATAA 206
Qy 131 ATAAATCCATCAGAAATGACACTTCTCAGGTGCTCTTGAATTAAGAGGAATCTTTTAC 190
Db 207 ATAAATCCATCAGAAATGACACTTCTCAGGTGCTCTTGAATTAAGAGGAATCTTTTAC 266
Qy 191 CAGGAGAAATTTTTCGATATGTGGAAGCTGTGATGCTTTTGGGAAACTGGAATCCTCAAA 250
Db 267 CAGGAGAAATTTTTCGATATGTGGAAGCTGTGATGCTTTTGGGAAACTGGAATCCTCAAA 326
Qy 251 ATGCTGTGGCTCTTCTCCAGAGATGACACAGGTGAAAGCATGCTATGAAAGCAACCA 310
Db 327 ATGCTGTGGCTCTTCTCCAGAGATGACACAGGTGAAAGCATGCTATGAAAGCAACCA 386
Qy 311 TTGTACTCAGTAGAGGATATCAGTTTCAATATCGTACTTCAAGGGTACTTTTTAGAAC 370
Db 387 TTGTACTCAGTAGAGGATATCAGTTTCAATATCGTACTTCAAGGGTACTTTTTAGAAC 446
Qy 371 CAAGACTATCGGTGCTCCATGTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC 430
Db 447 CAAGACTATCGGTGCTCCATGTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC 506
Qy 431 CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTTAGCAGTGGACAATTTGGAATCC 490
Db 507 CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTTAGCAGTGGACAATTTGGAATCC 566
Qy 491 ACAATGGTGTGAAACTCTGGATTCGATGCTGACATGTGACACTGGAATAGATTAC 550
Db 567 ACAATGGTGTGAAACTCTGGATTCGATGCTGACATGTGACACTGGAATAGATTAC 626
Qy 551 GTTTCGATTTCTGAAAACTCTCTGTCAATAACCAAGAAATAATTTAAAAAATCTA 610
Db 627 GTTTCGATTTCTGAAAACTCTCTGTCAATAACCAAGAAATAATTTAAAAAATCTA 686
Qy 611 GATTTAGGCTGAAGCTGACACTAGAAAGCCTGGAGGAAGATGACGATAGGGTATCTC 670
Db 687 GATTTAGGCTGAAGCTGACACTAGAAAGCCTGGAGGAAGATGACGATAGGGTATCTC 746
Qy 671 CCACGTACTCCAAAAATGTCAAATAGCTTGGAGATATCCTTAATAGCAGCAATGAT 730
Db 747 CCACGTACTCCAAAAATGTCAAATAGCTTGGAGATATCCTTAATAGCAGCAATGAT 806
Qy 731 TCAAGTGCAGGCATTTACAGCCGGAGTGGTTATGGCTTCAGCCTCATGCTTGGACAG 790
Db 807 TCAAGTGCAGGCATTTACAGCCGGAGTGGTTATGGCTTCAGCCTCATGCTTGGACAG 866
Qy 791 AGTACAGCATACAGAGATGGAACCAAGATAACCTTGGAACTAATCTTTGATTTTTTCGAAG 850
Db 867 AGTACAGCATACAGAGATGGAACCAAGATAACCTTGGAACTAATCTTTGATTTTTTCGAAG 926
Qy 851 AAGATCTCAGTAGCAGCAGTGTTCAGGGTGTATGCCCTTCCTGGA CATGGGGTACAGTT 910
Db 927 AAGATCTCAGTAGCAGCAGTGTTCAGGGTGTATGCCCTTCCTGGA CATGGGGTACAGTT 986
Qy 911 GTCTCTTATATCCACCATTTCTGAGAGTGGAAAGTGTGGATTTCTTACTCTTCCCA 970
Db 987 GTCTCTTATATATCCACCATTTCTGAGTGGAAAGTGTGGATTTCTTACTCTTCCCA 1046
Qy 971 TCATGAGCAGAAATTTCCGGAAAAAATAAGGCAGAGTGGAGTTGACTATATAATTA 1030
Db 1047 TCATGAGCAGAAATTTCCGGAAAAAATAAGGCAGAGTGGAGTTGACTATATAATTA 1106
Qy 1031 AGCCATTTACCAGGATACAGTTGTGACATGAATCTTTTCAATTTTCCAGTATTGGAAAGCAA 1090
Db 1107 AGCCATTTACCAGGATACAGTTGTGACATGAATCTTTTCAATTTTCCAGTATTGGAAAGCAA 1166
Qy 1091 GAATACCATTTGGATTTGGCCATCGAGGTGCAGGAAACTCTACAACACTGCCAGCTGG 1150
Db 1167 GAATACCATTTGGATTTGGCCATCGAGGTGCAGGAAACTCTACAACACTGCCAGCTGG 1226

Qy 1151 CTAAAGTTCAAGAAAAATACTATTGCTTCTTTAAGAAATGCTCTAGTCAATGCTGAGCCT 1210
Db 1227 CTAAAGTTCAAGAAAAATACTATTGCTTCTTTAAGAAATGCTCTAGTCAATGCTGAGCCT 1286
Qy 1211 TTGTAGAAATTCACGTACACCTTTCAAAGGACTTTTGTGCCCGTGGTATATCATGATCTTA 1270
Db 1287 TTGTAGAAATTCACGTACACCTTTCAAAGGACTTTTGTGCCCGTGGTATATCATGATCTTA 1346
Qy 1271 CTTGTTGTTTGAATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTC 1330
Db 1347 CTTGTTGTTTGAATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTC 1406
Qy 1331 CAGTAAAGAAATTAACATTTGACCAACTCCAGTTGTTAAAGCTCACTCAATGCTGAC 1390
Db 1407 CAGTAAAGAAATTAACATTTGACCAACTCCAGTTGTTAAAGCTCACTCAATGCTGAC 1466
Qy 1391 TGAATCTTAAGGATCGGAAGAAATCTGTGTTTTCAGGAGGAAATTCCTTTTTCAGAAAAATC 1450
Db 1467 TGAATCTTAAGGATCGGAAGAAATCTGTGTTTTCAGGAGGAAATTCCTTTTTCAGAAAAATC 1526
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Db 1527 AGCCATTTCTTCTCTTAAGATGTTTGTAGAGTCTTTTGCAGAGATGTAGGGTTTAAACA 1586
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Db 1587 TTGAATTAAGATGATCTCGCAGCAAGGATGGAATGTGGATGTTAACTTATCAACAT 1646
Qy 1571 ATTTTCACATGATCTGTTTTTTTGGATATAATTTTAAAAAATCTGTTTTTGAATAATCTCGGGA 1630
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Qy 1811 TGGGGATAAATGACATACATGTAAGAGACTTGTCTCAGAAACCCCATCTTATTTCAAGAGGCAA 1870
Db 1887 TGGGGATAAATGACATACATGTAAGAGACTTGTCTCAGAAACCCCATCTTATTTCAAGAGGCAA 1946
Qy 1871 AAGCTAAGGACTAGTCAATATCTGCTGGGGTGCATATCAATGATCCTTGAAAAACAGAA 1930
Db 1947 AAGCTAAGGACTAGTCAATATCTGCTGGGGTGCATATCAATGATCCTTGAAAAACAGAA 2006
Qy 1931 GGAATTTGAAGGAACTTGGAGTTAAATGGTCTAAATTTATGATAGGATATATGATTTGATGC 1990
Db 2007 GGAATTTGAAGGAACTTGGAGTTAAATGGTCTAAATTTATGATAGGATATATGATTTGATGC 2066
Qy 1991 CTGAACCAACCAATATATTTCCAAAGTGGAGCAATTTGAAACCCCTGAAGCAGGAAATTTGCCAG 2050
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Db 2127 AGCTTAAGAGCTGTTGTGTCTCCACTGTTAGCCGCTTTGTTCCCTCATCTTTTGTGTGGGG 2186
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Db 2187 AGCTGATATCCATGTCGATGCCAAACCGCATTTGATAACGTGGGAAATGCTTAGTTTTTAT 2246
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Db 2247 TGCAACAGAGGTCAATTTTGGGGGGTGCACCCGCTGTTCTGGGTATTTCAATTTTCAATCATG 2306

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Qy 431 CAGCATCAATCAACCCCTTTAGAGAGCGAAATTTATTTAGAGTGGACAATTTGGAATCC 490
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Qy 551 GTTTGCATTATCTGAAAAAAGCTCTGTGTCAATAAACAAGAAAAAATTTAAAAAATCTA 610
Db 627 GTTTGCATTATCTGAAAAAAGCTCTGTGTCAATAAACAAGAAAAAATTTAAAAAATCTA 686
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Qy 1571 ATTTTGACATGAATCTGTTTTTGGGATATAATTTTAAAAAAGCTTTTAAAAAATCTGGGA 1630
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Db 2006 GGAAATTTGAAGAACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATGATGATC 2065
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Db 1627 GCAAGTATGCTATTTAAATTAATCTTGGCCAGGTATTAATTTGCCAGTCAGTCTCTTTATAGTG 1686
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Qy 2552 TGCATATTTATATACCTGACCAATGAAATTAAGTAACTCAAAATGCAATGCAATTTGCACCTG 2611
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Qy 2612 TGAATTCACCTGACCAAAATCTTTGCGCATCTTGATATAGGTATTTTACATGCGGTTG 2671
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Db 2467 CATGCAGAAAAATTAATGCTGCTGAATTTCTCATA 2499

RESULT 10
ADJ57931
ID ADJ57931 standard; cDNA; 2738 BP.
XX
AC ADJ57931;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human NARC 9 cDNA.
XX

KW Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
 KW lung disease; cirrhosis; hepatitis; atherosclerosis;
 KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
 KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
 KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;
 KW drug screening; gene therapy; cytostatic; hepatotropic; neurotropic;
 KW cerebroprotective; dermatological; virucide; neuroprotective;
 KW phosphatidylglycerolphosphate synthase; PGP synthase; human; ss.
 XX Homo sapiens.
 XX US2004009553-A1.
 XX 15-JAN-2004.
 XX 30-APR-2003; 2003US-00426776.
 XX 27-SRP-1999; 99US-00406045.
 XX 22-OCT-1999; 99US-0161188P.
 XX 31-JAN-2000; 2000US-00495823.
 XX 28-FEB-2000; 2000US-0185517P.
 XX 20-OCT-2000; 2000US-00692785.
 XX 31-JAN-2001; 2001US-00773426.
 XX 28-FEB-2001; 2001US-00795691.
 XX 31-OCT-2001; 2001US-0335003P.
 XX 31-OCT-2001; 2001US-0335037P.
 XX 25-MAR-2002; 2002US-00105992.
 XX 28-AUG-2002; 2002US-00229662.
 XX 30-OCT-2002; 2002US-00284014.
 XX 30-OCT-2002; 2002US-00284059.
 XX 09-DEC-2002; 2002US-00314881.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Glucksmann MA, Williamson MJ, Tsai F, Rudolph-Owen LA;
 PI Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
 XX WPI; 2004-0904659/09.
 XX New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413,
 PT 22438, 23553, NARC SCl or NARC 1) useful for diagnosing, preventing or
 PT treating disorders associated with the protein, e.g. cancer,
 PT atherosclerosis or AIDS.
 XX Claim 1; SEQ ID NO 32; 260pp; English.
 XX The present invention provides isolated nucleic acid molecules and
 CC proteins designated 27411, 23413, 22438, 23553, 25278, NARC SCl,
 CC NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4,
 CC NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20,
 CC NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C,
 CC NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or
 CC 32222. The invention is useful in diagnosing, preventing or treating
 CC disorders such as cancer; lung diseases, cirrhosis, hepatitis,
 CC atherosclerosis, myocardial infarction, inflammation, anaemia,
 CC glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency
 CC syndrome), Parkinson's disease, Alzheimer's disease, stroke and
 CC dermatitis. These may also be used in drug screening. The invention is
 CC also useful in gene therapy. The present sequence is human neuronal
 CC apoptosis regulated candidate (NARC) cDNA.
 XX Sequence 2738 BP; 880 A; 450 C; 540 G; 868 T; 0 U; 0 Other;
 SQ
 Query Match 77.4%; Score 2481.8; DB 12; Length 2738;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2486; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 692 CCAATAGCTTGAGATATCTTAATAAGCGACAATGATGATCAAGTCGAGCGATTACACAGC 751
 DB 7 CCACGGCTCCGAGATATCTTAATAAGCGACAATGATGATCAAGTCGAGCGATTACACAGC 66
 QY 752 CGAGTGTGGTATGGCTTGACGCTGATCGTTGACAGAGTACAGCATACAGAGTGG 811

Db 67 CGAGTGTGGTATAGCTTGGCTTGGAGCCTGATCGTGTGGAAGAGTACAGCATACAGAGTGG 126
 QY 812 AACACAGATAAACCCTGGAACCTAATCTTTTGGATTTTTCGAAAGAGATCTCAGTGCAGCAGTAG 871
 Db 127 AACACAGATAAACCCTGGAACCTAATCTTTTGGATTTTTCGAAAGAGATCTCAGTGCAGCAGTAG 186
 QY 872 TTCAGGGTATGCCCTTCTCTGGAACATGTTGGGTACAGCTTGTCTTATCATCCACCATG 931
 Db 187 TTCAGGGTATGCCCTTCTCTGGAACATGTTGGGTACAGCTTGTCTTATCATCCACCATG 246
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 Db 247 CTGACAGTGGAAAGAGTGTCTGGAATTTCTTACTCTTCCCATCATGAGCAGAAATCCCGGA 306
 QY 992 AAACAATAGGCAAGTGTGAGATGTACTATATAATTAATTAAGCCATTACAGGATACAGTT 1051
 Db 307 AAACAATAGGCAAGTGTGAGATGTACTATATAATTAATTAAGCCATTACAGGATACAGTT 366
 QY 1052 GTGACATGAATCTTTCATTTTCCAAAGTATTTGGAAGCCAAAGATACCATTTGATGTGGCC 1111
 Db 367 GTGACATGAATCTTTCATTTTCCAAAGTATTTGGAAGCCAAAGATACCATTTGATGTGGCC 426
 QY 1112 ATCGAGTGCAGGAACTCTACAACTGCCAGCTGGCTAAGTTTCAAGAAATACATA 1171
 Db 427 ATCGAGTGCAGGAACTCTACAACTGCCAGCTGGCTAAGTTTCAAGAAATACATA 486
 QY 1172 TTGCTTTCTTAAAGAAATGCTGTAGTATCATGTATCATGATCTTACCTGTTGTTGATGAAGA 1231
 Db 487 TTGCTTTCTTAAAGAAATGCTGTAGTATCATGTATCATGATCTTACCTGTTGTTGATGAAGA 546
 QY 1232 TTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGATGAAGA 1291
 Db 547 TTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGATGAAGA 606
 QY 1292 AGAAATTTGATGCTGATCCAGTTCGAATTTTGAATTTCCAGTAAAGAAATTAACATTTG 1351
 Db 607 AGAAATTTGATGCTGATCCAGTTCGAATTTTGAATTTCCAGTAAAGAAATTAACATTTG 666
 QY 1352 ACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGGATCGGAAG 1411
 Db 667 ACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGGATCGGAAG 726
 QY 1412 AATCTGTGTTTCCAGAGGAAATTTCTTTTTCAGAAATTCAGCCATTTCTCTCTTAAGA 1471
 Db 727 AATCTGTGTTTCCAGAGGAAATTTCTTTTTCAGAAATTCAGCCATTTCTCTCTTAAGA 786
 QY 1472 TGGTTTATAGTCTTTGCCAGAGATGTAGGGTTTAAATTTGAATTTAAATTTGATCTGCC 1531
 Db 787 TGGTTTATAGTCTTTGCCAGAGATGTAGGGTTTAAATTTGAATTTAAATTTGATCTGCC 846
 QY 1532 AGCAAGGGATGGAATGTGGATGTTAACTTATCAACATATTTTGACATGAATCTGTTTT 1591
 Db 847 AGCAAGGGATGGAATGTGGATGTTAACTTATCAACATATTTTGACATGAATCTGTTTT 906
 QY 1592 TGGATATAATTTTAAAACTGTTTTTAGAAAAATCTCGGAAGAGGAGAAATAGTGTGTTTT 1651
 Db 907 TGGATATAATTTTAAAACTGTTTTTAGAAAAATCTCGGAAGAGGAGAAATAGTGTGTTTT 966
 QY 1652 CATTTGATGAGATATTTGCAATGTTTGGGCAAAAGCAGAAATATCCGATATCAT 1711
 Db 967 CATTTGATGAGATATTTGCAATGTTTGGGCAAAAGCAGAAATATCCGATATCAT 1026
 QY 1712 TTTTAACTCAAGGAAATCTGAGATTTTATCTGAATCTCATGACCTCAGATCTCGGACAA 1771
 Db 1027 TTTTAACTCAAGGAAATCTGAGATTTTATCTGAATCTCATGACCTCAGATCTCGGACAA 1086
 QY 1772 CCCCATTGCAATGAGCTTTTGCACAGTTTGAATACTTCTGCGGATAAATGTACATCTG 1831
 Db 1087 CCCCATTGCAATGAGCTTTTGCACAGTTTGAATACTTCTGCGGATAAATGTACATCTG 1146
 QY 1832 AAGACTTGTCTCAGAAACCCATCTTATTTCAAGAGGCAAAAGCTAAGGAGCTAGTCTAT 1891
 Db 1147 AAGACTTGTCTCAGAAACCCATCTTATTTCAAGAGGCAAAAGCTAAGGAGCTAGTCTAT 1206

CC suitable for binding of the test compound to the polypeptide. The method
CC of the invention has haematological and cytostatic applications and may
CC be useful for identifying compounds for treating a haematological
CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
CC identified may be utilised during gene therapy procedures. The current
CC sequence is that of a human haematological disorder-related cDNA of the
CC invention.

XX
SQ Sequence 2019 BP; 633 A; 363 C; 449 G; 574 T; 0 U; 0 Other;

Query Match 53.0%; Score 2019; DB 13; Length 2019;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	145	ATGACACCTTCTCAGCTGGCTTTGAAATAAGAGGAACCTCTTTACGAGGAAAGTTTTT	204
DB	1	ATGACACCTTCTCAGCTGGCTTTGAAATAAGAGGAACCTCTTTACGAGGAAAGTTTTT	60
QY	205	GGGATATGGAGCTGTGATGCTTTGGGAAACTCGGAATCCTCAAAATCTGTGGCTCTT	264
DB	61	GGGATATGGAGCTGTGATGCTTTGGGAAACTCGGAATCCTCAAAATCTGTGGCTCTT	120
QY	265	CTTCAGAGATGACACAGGTGAAGCATGCTATGGAAGCAACCACTGTACTCAGTAGA	324
DB	121	CTTCAGAGATGACACAGGTGAAGCATGCTATGGAAGCAACCACTGTACTCAGTAGA	180
QY	325	GGAGTATCAGTTCAGTATCGTACTTTCAAGGGTACTTTTGAACCAAGACTATCGGT	384
DB	181	GGAGTATCAGTTCAGTATCGTACTTTCAAGGGTACTTTTGAACCAAGACTATCGGT	240
QY	385	GGTCCATGTCAAGTGTAGTTCACAGTGGGAGACTCATCTCAACACGATCAATAACC	444
DB	241	GGTCCATGTCAAGTGTAGTTCACAGTGGGAGACTCATCTCAACACGATCAATAACC	300
QY	445	CCTTTAGAAAGCGAAATTAATTAATGACGATGACAAATTTGGAATCACAATGGTGTGAA	504
DB	301	CCTTTAGAAAGCGAAATTAATTAATGACGATGACAAATTTGGAATCACAATGGTGTGAA	360
QY	505	ACTCTGGATCTCGGATGGCTGACATGTCAGACTGAAATGAAGATTAGTTGCATTTCT	564
DB	361	ACTCTGGATCTCGGATGGCTGACATGTCAGACTGAAATGAAGATTAGTTGCATTTCT	420
QY	565	GAAAAACCTCTGTGTCAATAACCAAGAAAAAATTAAGAAATCTAGATTTAGGGTGAAG	624
DB	421	GAAAAACCTCTGTGTCAATAACCAAGAAAAAATTAAGAAATCTAGATTTAGGGTGAAG	480
QY	625	CTGACACTAGAGGCTCGGAGGAAGATGACGATAGGGTATCTCCCACTGTACTCCAC	684
DB	481	CTGACACTAGAGGCTCGGAGGAAGATGACGATAGGGTATCTCCCACTGTACTCCAC	540
QY	685	AAATGTCCAATAGCTTGAGATATCCTTAATAGCGACAATGAGTTCAAGTGCAGGCAT	744
DB	541	AAATGTCCAATAGCTTGAGATATCCTTAATAGCGACAATGAGTTCAAGTGCAGGCAT	600
QY	745	TCACAGCCGAGTGTGGTTATGGCTTGACGCTGATCGTTGGACAGATACAGCATACAG	804
DB	601	TCACAGCCGAGTGTGGTTATGGCTTGACGCTGATCGTTGGACAGATACAGCATACAG	660
QY	805	ACGATGGAAACCGATAACCTGGAACTTAATCTTTGATTTTTTCAAGAGATCTCAGTAG	864
DB	661	ACGATGGAAACCGATAACCTGGAACTTAATCTTTGATTTTTTCAAGAGATCTCAGTAG	720
QY	865	CACGTAGTTACGGGTGATGCCCTTCTGACATGCGGTACAGCTGTCTTATCATCC	924
DB	721	CACGTAGTTACGGGTGATGCCCTTCTGACATGCGGTACAGCTGTCTTATCATCC	780
QY	925	ACCATTTGCTGAGATGGAAAGAGTGTGGAAATCTTACTCTTCCCATCATGAGCAGAAAT	984
DB	781	ACCATTTGCTGAGATGGAAAGAGTGTGGAAATCTTACTCTTCCCATCATGAGCAGAAAT	840
QY	985	TCCCGGAAAAACAATAGGCAAGGTGAGTTGACTATATAATTAATTAAGCCATTACCAGGA	1044

DB	841	TCCCGGAAAAACAATAGGCAAGGTGAGTTGACTATATAATTAATTAAGCCATTACCAGGA	900
QY	1045	TACAGTTGTGACATCAAAATCTTCAATTTTCCAAGTATTGGAAGCCCAAGAAATCACTTGGAT	1104
DB	901	TACAGTTGTGACATCAAAATCTTCAATTTTCCAAGTATTGGAAGCCCAAGAAATCACTTGGAT	960
QY	1105	GTGCGCCATCGAGGTGCGAGGAAACTCTACAACACTGCCAGCTGGCTTAAAGTTCAAGAA	1164
DB	961	GTGCGCCATCGAGGTGCGAGGAAACTCTACAACACTGCCAGCTGGCTTAAAGTTCAAGAA	1020
QY	1165	AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAATGCTGAGCCTTTGTAGAAATTCAC	1224
DB	1021	AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAATGCTGAGCCTTTGTAGAAATTCAC	1080
QY	1225	GTACACCTTTCAAGAGACTTTGTGCCCGTGTATATCATGATCTTACCTGTGTGTGACT	1284
DB	1081	GTACACCTTTCAAGAGACTTTGTGCCCGTGTATATCATGATCTTACCTGTGTGTGACT	1140
QY	1285	ATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTTCCAGTAAAGAAATTA	1344
DB	1141	ATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTTCCAGTAAAGAAATTA	1200
QY	1345	ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGAT	1404
DB	1201	ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGAT	1260
QY	1405	CGGAAAGAAATCTGTGGTTTCAGAGGAAATTTCTTTTCAGAAAAATCAGCCATTTCTTCT	1464
DB	1261	CGGAAAGAAATCTGTGGTTTCAGAGGAAATTTCTTTTCAGAAAAATCAGCCATTTCTTCT	1320
QY	1465	CTTAAGATGGTTTTAGAGTCTTTTGCAGAGATGTAGGGTTTTAATTAAGAAATTAAGTGG	1524
DB	1321	CTTAAGATGGTTTTAGAGTCTTTTGCAGAGATGTAGGGTTTTAATTAAGAAATTAAGTGG	1380
QY	1525	ATCTGCCAGAAAGGGATGGAAATGTGGATGGTAACTTTATCAACATATTTTTCACATGAAT	1584
DB	1381	ATCTGCCAGAAAGGGATGGAAATGTGGATGGTAACTTTATCAACATATTTTTCACATGAAT	1440
QY	1585	CTGTTTTTGGATATAATTTTAAAGAACTGTTTTAGAAAAATCTGGAAGAGGAGATAGTG	1644
DB	1441	CTGTTTTTGGATATAATTTTAAAGAACTGTTTTAGAAAAATCTGGAAGAGGAGATAGTG	1500
QY	1645	TTTTCTTCATTTGATGACAGATATTTGCAAAATGGTTTCGCAAAAAGCAGAAATATCCG	1704
DB	1501	TTTTCTTCATTTGATGACAGATATTTGCAAAATGGTTTCGCAAAAAGCAGAAATATCCG	1560
QY	1705	ATACTATTTTAACTCAAGGAAATCTGAGATTTTATCTGAACTCATGGACCTCAGATCT	1764
DB	1561	ATACTATTTTAACTCAAGGAAATCTGAGATTTTATCTGAACTCATGGACCTCAGATCT	1620
QY	1765	CGGCAACCCCATTTGCAATGAGCTTTTGCACAGTTTGAATAATCTACTGGGATATAATGTA	1824
DB	1621	CGGCAACCCCATTTGCAATGAGCTTTTGCACAGTTTGAATAATCTACTGGGATATAATGTA	1680
QY	1825	CATCTGAAGACTTGTCTCAGAAACCCATCTTATATTTCAAGAGGCAAAAGCTTAAGGACTA	1884
DB	1681	CATCTGAAGACTTGTCTCAGAAACCCATCTTATATTTCAAGAGGCAAAAGCTTAAGGACTA	1740
QY	1885	GTCAATTTCTGCTGGGTGATGATACCAATGATCTGAAAAACAGAGGAAATTTGAAGAA	1944
DB	1741	GTCAATTTCTGCTGGGTGATGATACCAATGATCTGAAAAACAGAGGAAATTTGAAGAA	1800
QY	1945	CTTCGAGTTAATGCTTAATTTATGATAGGATATATGATTTGGATGCTTGAACCAAT	2004
DB	1801	CTTCGAGTTAATGCTTAATTTATGATAGGATATATGATTTGGATGCTTGAACCAAT	1860
QY	2005	ATATTTCAAAGTGGAGCAATTTGAAACCGCTGAAGCAGGAAATTTGCCAGAGCTTTAAGAGCTGT	2064
DB	1861	ATATTTCAAAGTGGAGCAATTTGAAACCGCTGAAGCAGGAAATTTGCCAGAGCTTTAAGAGCTGT	1920
QY	2065	TTGTGTCCCACTGTAGCCGCTTTGTTCCTCATCTTTGTGTGGGGAGTCTGATATCCAT	2124

Db 1921 TTGTGTCCTCACTGTAGCGCTTTTGTCCCTCATCTTTGTGTGGGAGTCTGATATCCAT 1980

QY 2125 GTGATGCCAAGCGCATTTGATAAAGTGGAGAAATGCTTAG 2163

Db 1981 GTGGATGCCAAGCGCATTTGATAAAGTGGAGAAATGCTTAG 2019

RESULT 12

AAH14905

ID AAH14905 standard; cDNA; 1803 BP.

XX AC AAH14905;

XX 26-JUN-2001 (first entry)

XX Human cDNA sequence SEQ ID NO:12778.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 12778; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention

XX Sequence 1803 BP; 561 A; 291 C; 355 G; 596 T; 0 U; 0 Other;

Query Match 56.2%; Score 1803; DB 4; Length 1803;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Matches 1803; Conservative 0;

QY 1379 ATGTGACTGCACCTGAAATCTAAGGATCGGAAAGAAATCTGTGGTTCAGGAGGAAATTCCT 1438

Db 1 ATGTGACTGCACCTGAAATCTAAGGATCGGAAAGAAATCTGTGGTTCAGGAGGAAATTCCT 60

QY 1439 TTTCAGAAATCAGCCATTTCTTCTTAAGATGTTTTAGAGTCTTTTGCCAGAGAATG 1498

Db 61 TTTCAGAAATCAGCCATTTCTTCTTAAGATGTTTTAGAGTCTTTTGCCAGAGAATG 120

QY 1499 TAGGGTTTAAACATTGAAATAAATAATGGATCTGCCAGCAAGGGATGGAATGTGGATGGTA 1558

Db 121 TAGGGTTTAAACATTGAAATAAATAATGGATCTGCCAGCAAGGGATGGAATGTGGATGGTA 180

QY 1559 ACTTATCAACATATTTTGACATGAATCTGTGTGGATGATAAATTTTAAACCTGTTTTAG 1618

Db 181 ACTTATCAACATATTTTGACATGAATCTGTGTGGATGATAAATTTTAAACCTGTTTTAG 240

QY 1619 AAAATTTCTGGAGAGGAGGAGATAGTGTTCCTTCATTTGATCGAGATATTTGACAAATGG 1678

Db 241 AAAATTTCTGGAGAGGAGGAGATAGTGTTCCTTCATTTGATCGAGATATTTGACAAATGG 300

QY 1679 TTGGCAAAAGCAGAACAAATATCCGATATCTATTTTAACTCAAGGAAATCTGAGATTT 1738

Db 301 TTGGCAAAAGCAGAACAAATATCCGATATCTATTTTAACTCAAGGAAATCTGAGATTT 360

QY 1739 ATCTGAACTCATGGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCTTTGCAAGT 1798

Db 361 ATCTGAACTCATGGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCTTTGCAAGT 420

QY 1799 TTGAAATCTACTGGGGATAAATGTACATCTGAAAGCTTGTCTCAGAAACCCCACTATA 1858

Db 421 TTGAAATCTACTGGGGATAAATGTACATCTGAAAGCTTGTCTCAGAAACCCCACTATA 480

QY 1859 TTCAAGAGGCAAAAGCTTAAGGGACTAGTCATATTTCTGCTGGGTGATGATACCAATGATC 1918

Db 481 TTCAAGAGGCAAAAGCTTAAGGGACTAGTCATATTTCTGCTGGGTGATGATACCAATGATC 540

QY 1919 CTGAAACAGAGGAAATTTGAAGGAATCTGGAGTAAATGGTCTTAATTTATGATAGGATAT 1978

Db 541 CTGAAACAGAGGAAATTTGAAGGAATCTGGAGTAAATGGTCTTAATTTATGATAGGATAT 600

QY 1979 ATGATGGATGCTGAAACCAACCAATATATTCGAAGTGGAGCAATTTGGAACGCTGAGC 2038

Db 601 ATGATGGATGCTGAAACCAACCAATATATTCGAAGTGGAGCAATTTGGAACGCTGAGC 660

QY 2039 AGGAATTTGCCAGAGCTTAAGAGCTTTGTGTCCCACTGTAGCCGCTTTTGTTCCTTCAT 2098

Db 661 AGGAATTTGCCAGAGCTTAAGAGCTTTGTGTCCCACTGTAGCCGCTTTTGTTCCTTCAT 720

QY 2099 CTTTGTCTGGGAGTCTGATATCCATGTGATGCAACGGCATTTGATTAACGTGGAGAATG 2158

Db 721 CTTTGTCTGGGAGTCTGATATCCATGTGATGCAACGGCATTTGATTAACGTGGAGAATG 780

QY 2159 CTTAGTTTTTATTTGACAGAGGTCAATTTGGGGCGTGCACCGCTGTTTGGGGTATTCAT 2218

Db 781 CTTAGTTTTTATTTGACAGAGGTCAATTTGGGGCGTGCACCGCTGTTTGGGGTATTCAT 840

QY 2219 TTTTCATCAGTGGATTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAGCAAT 2278

Db 841 TTTTCATCAGTGGATTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAGCAAT 900

QY 2279 AATGAAGTTTAACTCTTTTCACTACAGTCTTTGCAAGTATGCTATTAAATTAATTTGGC 2338

Db 901 AATGAAGTTTAACTCTTTTCACTACAGTCTTTGCAAGTATGCTATTAAATTAATTTGGC 960

QY 2339 CAGGTATAATTTGCCAGTCAGTCTCTTTTATAGTGAGAAATTTATTTGTTAGTATATAAA 2398

Db 961 CAGGTATAATTTGCCAGTCAGTCTCTTTTATAGTGAGAAATTTATTTGTTAGTATATAAA 1020

QY 2399 TATTTTAACTAAATATATAAATCTAATGTTTAAACATATGTTTCAATTAAGCATAGCA 2458

Db 1021 TATTTAACTAATATATAATCTATAATGTTAAACATATGTTCAATAAAGCATAGCA 1080
Qy 2459 CTTTGAAATTAACATATAATAAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGG 2518
Db 1081 CTTTGAAATTAACATATAATAAGCTCATATTTACACTTACAGCTTTTCATTTGATCAGG 1140
Qy 2519 TCTGAATCTTTAGCACTTAAGGAAATGACTATGCTAATATTAATCTGACCAATGAAAA 2578
Db 1141 TCTGAATCTTTAGCACTTAAGGAAATGACTATGCTAATATTAATCTGACCAATGAAAA 1200
Qy 2579 AATAAGTACCTCAAAATGATGCTATTTGCACTGCTGATTTCCAACTGCACAAATCTTTGTGC 2638
Db 1201 AATAAGTACCTCAAAATGATGCTATTTGCACTGCTGATTTCCAACTGCACAAATCTTTGTGC 1260
Qy 2639 CATCTGTATATAGGTATTTTACATGGTGTGACATGACACAAACCACTTTTCATTTCA 2698
Db 1261 CATCTGTATATAGGTATTTTACATGGTGTGACATGACACAAACCACTTTTCATTTCA 1320
Qy 2699 GTATGAACCTTGAGGCTGCTGCCATTTTCCACTTAACCAACCAAGCTGAAGGTGAAC 2758
Db 1321 GTATGAACCTTGAGGCTGCTGCCATTTTCCACTTAACCAACCAAGCTGAAGGTGAAC 1380
Qy 2759 TCGAAATCTGTTTCATAAATCTTTCAAAAGTCTGTTTACATCAATGTTAAATTTTCAAA 2818
Db 1381 TCGAAATCTGTTTCATAAATCTTTCAAAAGTCTGTTTACATCAATGTTAAATTTTCAAA 1440
Qy 2819 TCGTCAAGGTAAATTAATGTATAAATAATTAAGTAAAGAAAGTATGTTATGCACTTA 2878
Db 1441 TCGTCAAGGTAAATTAATGTATAAATAATTAAGTAAAGAAAGTATGTTATGCACTTA 1500
Qy 2879 GTAGATAGATCAACATACAAATTCATTCAGTGCATGCTTTAGGTGTTAAGCATGAG 2938
Db 1501 GTAGATAGATCAACATACAAATTCATTCAGTGCATGCTTTAGGTGTTAAGCATGAG 1560
Qy 2939 ATTGTACATGTTTACTGTTAGTCCCTTGCATCTGCTGCTAGTGCAGTATGAGAGATG 2998
Db 1561 ATTGTACATGTTTACTGTTAGTCCCTTGCATCTGCTGCTAGTGCAGTATGAGAGATG 1620
Qy 2999 TCAAGACTGGACGTTATTTGTTGCTTAAATAAAGGCTGTTTGTAGCGCTTTTAAAT 3058
Db 1621 TCAAGACTGGACGTTATTTGTTGCTTAAATAAAGGCTGTTTGTAGCGCTTTTAAAT 1680
Qy 3059 ATGCTTAATTTGTTGCTCTCACTACCTATTACACACTGTTGCTTTGGGTTTGTGTTT 3118
Db 1681 ATGCTTAATTTGTTGCTCTCACTACCTATTACACACTGTTGCTTTGGGTTTGTGTTT 1740
Qy 3119 GTATGCGTGTGTTATACAGTAGTTTAAATTTCCATGCAGAAAAATAAATGCTCGAAT 3178
Db 1741 GTATGCGTGTGTTATACAGTAGTTTAAATTTCCATGCAGAAAAATAAATGCTCGAAT 1800
Qy 3179 CTC 3181
Db 1801 CTC 1803

RESULT 13
AAH44173

XX AAH44173 standard; cDNA; 1929 BP.

AC AAH44173;

XX 21-SEP-2001 (first entry)

DE Human glycerophosphodiesterase 25 encoding cDNA SEQ ID NO:1.

KW Human: glycerophosphodiesterase 25; cytostatic; anti-HIV; tumour;
KW immunomodulatory; antiinflammatory; haemopathy; HIV infection;
KW immunological disease; inflammation; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
FH 2..694
FT CDS

FT /*tag= a
FT /product= "glycerophosphodiesterase 25"

XX WO200146435-A1.

XX 28-JUN-2001.

XX 18-DEC-2000; 2000WO-CN000609.

XX 22-DEC-1999; 99CN-00125684.

XX (BIOW-) BLOWNDOW GENE DEV INC SHANGHAI.

PI Mao Y, Xie Y;

XX WPI: 2001-418073/44.

DR P-PSDB; AAB99775.

XX Human glycerophosphodiesterase 25 and encoded polynucleotide, applicable
PT in diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation.

XX Claim 6; Page 31-32; 37pp; Chinese.

CC The present sequence encodes the human glycerophosphodiesterase 25
CC protein (I). (II) and the polynucleotide sequence encoding it (II) are
CC applicable in the diagnosis and treatment of malignant tumour,
CC haemopathy, HIV infection, immunological diseases and various
CC inflammation. (I) has cytostatic, anti-HIV, immunomodulatory and
CC antinflammatory activities. (II) is also useful for screening mimics,
CC agonists, antagonists or inhibitors, or for use in peptide fingerprinting
CC identification. The polynucleotide can be used as primers for nucleic
CC acid amplification reaction or as probes for hybridisation reaction, or
CC in producing gene chips or microarrays

XX Sequence 1929 BP; 608 A; 298 C; 372 G; 651 T; 0 U; 0 Other;

Query Match 53.0%; Score 1698.2; DB 4; Length 1929;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1711; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1470 GATGGTTTATAGAGCTTTTCCAGAGATGATGGGTTTAAACATTGAAATGATCTGTT 1529

Db 1 GATGGTTTATAGAGCTTTTCCAGAGATGATGGGTTTAAACATTGAAATGATCTGTT 60

Qy 1530 CCAGCAAGGATGGAATGTTGGGATGTTTAACTTATCAATATTTTCACATGATCTGTT 1589

Db 61 CCAGCAAGGATGGAATGTTGGGATGTTTAACTTATCAATATTTTCACATGATCTGTT 120

Qy 1590 TTTGGATATATTTTAAATAAATCTGTTTAAATAAATCTGTTGGGAGAGGAGATGTTTTC 1649

Db 121 TTTGGATATATTTTAAATAAATCTGTTTAAATAAATCTGTTGGGAGAGGAGATGTTTTC 180

Qy 1650 TTCAATTTATGTCAGATATTTGCAATGTTTGGCAAAAGCAGAAATATCCGATCT 1709

Db 181 TTCAATTTATGTCAGATATTTGCAATGTTTGGCAAAAGCAGAAATATCCGATCT 240

Qy 1710 ATTTTAACTCAAGGAAATCTGAGATTTATCCTGAACTCATGACCTCAGATCTCGAC 1769

Db 241 ATTTTAACTCAAGGAAATCTGAGATTTATCCTGAACTCATGACCTCAGATCTCGAC 300

Qy 1770 AACCCCAATTTGCAATGAGCTTTTGCACAGTTTGAATAATCTACTGGGATAAATGTACATAC 1829

Db 301 AACCCCAATTTGCAATGAGCTTTTGCACAGTTTGAATAATCTACTGGGATAAATGTACATAC 360

Qy 1830 TGAAGACTTGTCTAGAAACCCATCTTATATTCAGAGGCAAAAGCTAAGGACTAGTCTAT 1889

Db 361 TGAAGACTTGTCTAGAAACCCATCTTATATTCAGAGGCAAAAGCTAAGGACTAGTCTAT 420

Qy 1890 ATTCTGCTGGGGTGATGATACCAATGATCTCTGAAACAGAGGAAATTTGAAGNACTGG 1949

Db 421 ATTCTGCTGGGGTGATGATACCAATGATCTCTGAAACAGAGGAAATTTGAAGNACTGG 480

QY	1950	AGTTAATGGTCTAAATTTATGATAGGATATATGATTGGATGCTGCAACCAACCAATATATT	2009
DB	481	AGTTAATGGTCTAAATTTATGATAGGATATATGATTGGATGCTGCAACCAACCAATATATT	540
QY	2010	CCAAGTGGAGCAATTTGGAACCGCTGAAGCAGGAATTTGCCAGAGCTTTAAGAGCTGTTTGTG	2069
DB	541	CCAAGTGGAGCAATTTGGAACCGCTGAAGCAGGAATTTGCCAGAGCTTTAAGAGCTGTTTGTG	600
QY	2070	TCCCATGTTAGCGGCTTTGTTCCCTCATCTTTTGTTGGGGAGTCTGATATCCAGTGTGA	2129
DB	601	TCCCACTGTTAGCGGCTTTGTTCCCTCATCTTTTGTTGGGGAGTCTGATATCCAGTGTGA	660
QY	2130	TGCCAAGCGGCAATTTGATACCTGAGAGATGCTTAGTATTTTATTGTGCAAGAGGTCATTTGG	2189
DB	661	TGCCAAGCGGCAATTTGATACCTGAGAGATGCTTAGTATTTTATTGTGCAAGAGGTCATTTGG	720
QY	2190	GGGCGTGCACCGCTGTTTCTGGGTATTCATTTTTTCACTACGTAGCATTTGTGTATCTATGCC	2249
DB	721	GGGCGTGCACCGCTGTTTCTGGGTATTCATTTTTTCACTACGTAGCATTTGTGTATCTATGCC	780
QY	2250	TTTTGGGCTCTCTCAGTTTCAATGAAGCAATAATCAAGTATTTTAACTCTTTTCACTACAGTTTC	2309
DB	781	TTTTGGGCTCTCTCAGTTTCAATGAAGCAATAATCAAGTATTTTAACTCTTTTCACTACAGTTTC	840
QY	2310	TTGCAAGTATGCTATTTTAAATTTACTTGGCCAGGTATAAATGCCAGTCAGTCTCTTTTATAG	2369
DB	841	TTGCAAGTATGCTATTTTAAATTTACTTGGCCAGGTATAAATGCCAGTCAGTCTCTTTTATAG	900
QY	2370	TGAGAAAAATTTATTTGGTTAGTAAATATAAATAATTTTTTAACTAAATATATAAATCTATAATG	2429
DB	901	TGAGAAAAATTTATTTGGTTAGTAAATATAAATAATTTTTTAACTAAATATATAAATCTATAATG	960
QY	2430	TTAAACATATGTTTCAATTAARAGCATGCACTTTTGAATTTAACTATATAAATAGCTCATAT	2489
DB	961	TTAAACATATGTTTCAATTAARAGCATGCACTTTTGAATTTAACTATATAAATAGCTCATAT	1020
QY	2490	TTACACTTTACAGCTTTTTCATTTGATCAGGCTCTGAAATCTTTTAGCACCTTAAGGAAAAATGAC	2549
DB	1021	TTACACTTTACAGCTTTTTCATTTGATCAGGCTCTGAAATCTTTTAGCACCTTAAGGAAAAATGAC	1080
QY	2550	TATGCATAAATTTATACCTGACCATGAAAAAATAAGTACCTCAAAATGCATGCACTTTGCACCT	2609
DB	1081	TATGCATAAATTTATACCTGACCATGAAAAAATAAGTACCTCAAAATGCATGCACTTTGCACCT	1140
QY	2610	GGTGATTCCTCAACTGCACAAATCTTTGTGCCACTTTGTATATAGTATTTTTTACATCGGGT	2669
DB	1141	GGTGATTCCTCAACTGCACAAATCTTTGTGCCACTTTGTATATAGTATTTTTTACATCGGGT	1200
QY	2670	TGACATGCACACAAACACATTTTTCATTCAGTATGAACCTTTGAGGCTGCTGCCATTTTTTCC	2729
DB	1201	TGGCATGCACACACACATTTTTCATTCAGTATGAACCTTTGAGGCTGCTGCCATTTTTTCC	1260
QY	2730	ACTTAAACAAACCGCTGGAAGGTGAACCTCGAAACTTTGTTTCATAAATCTTTTCAAAGT	2789
DB	1261	ACTTAAACAAACCGCTGGAAGGTGAACCTCGAAACTTTGTTTCATAAATCTTTTCAAAGT	1320
QY	2790	TGTTTTTACATCAATGTTTAAATTTTCAAATGCTCGAGGTAATTTTAAATGATATAAATAATT	2849
DB	1321	TGTTTTTACATCAATGTTTAAATTTTCAAATGCTCGAGGTAATTTTAAATGATATAAATAATT	1380
QY	2850	AGTAAAGAAAAAGTATGTTATGTCATCTTTAGTAGAATAGATCACAAACATACAAATTCAAATT	2909
DB	1381	AGTAAAGAAAAAGTATGTTATGTCATCTTTAGTAGAATAGATCACAAACATACAAATTCAAATT	1440
QY	2910	CAGTGCATGCTTTAGGTGTTAAGCATGAGATGTTACATGTTTACTGTTAGGTCCTTCGAT	2969
DB	1441	CAGTGCATGCTTTAGGTGTTAAGCATGAGATGTTACATGTTTACTGTTAGGTCCTTCGAT	1500
QY	2970	CNTGCGTGTAGTGTAGATGAGAAAGATGTCGAAGCATGGAACGTATTTTGTGTGCTAAAA	3029
DB	1501	CTGTGCGTGTAGTGTAGATGAGAAAGATGTCGAAGCATGGAACGTATTTTGTGTGCTAAA	1559
QY	3030	AAAAAAGGCTGTTTGTAGCGGTTTTTAAATATGCTTATTTTTGTGTGCTCTCACTACCTAT	3089

Db	1560	AAAAAAGGCGTGTGTAGCGGTTTAAATATGCTTAATTTGTGTCTCTCACTACTAT	1619
Qy	3090	TACACACTGTTGCTTGTGGGTTTGTGTTGTATGTCGTTGTTATACAGTAGTAAAT	3149
Db	1620	TACACACTGTTGCTTGTGGGTTTGTGTTGTATGTCGTTGTTATACAGTAGTAAAT	1679
Qy	3150	TCCATGCAGAAAAATAAATGTCTCGAATTCTCAA	3184
Db	1680	TCCATGCAGAAAAATAAATGTCTCGAATTCTCAT	1714
RESULT 14			
ADJ57938			
ID	ADJ57938	standard; cDNA; 3381 BP.	
XX	AC	ADJ57938;	
XX	DT		
XX	06-MAY-2004	(first entry)	
XX	Rat	NARC 16 cDNA.	
XX	Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;		
XX	lung disease; cirrhosis; hepatitis; atherosclerosis;		
KW	myocardial infarction; inflammation; anaemia; glomerulonephritis;		
KW	osteoporosis; AIDS; acquired immunodeficiency syndrome;		
KW	Parkinson's disease; Alzheimer's disease; stroke; dermatitis;		
KW	drug screening; gene therapy; cytostatic; hepatotropic; nootropic;		
KW	cerebroprotective; dermatological; virucide; neuroprotective;		
KW	phosphatidylglycerolphosphate synthase; PGP synthase; rat; ss.		
XX	Rattus norvegicus.		
OS			
XX	US2004009553-A1.		
PN			
XX	15-JAN-2004.		
PD			
PF	30-APR-2003; 2003US-00426776.		
XX	27-SEP-1999; 99US-00406045.		
PR	22-OCT-1999; 99US-0161188P.		
PR	31-JAN-2000; 2000US-00495823.		
PR	28-FEB-2000; 2000US-0185517P.		
PR	20-OCT-2000; 2000US-00692785.		
PR	31-JAN-2001; 2001US-00773426.		
PR	28-FEB-2001; 2001US-00795691.		
PR	31-OCT-2001; 2001US-0335003P.		
PR	31-OCT-2001; 2001US-0335037P.		
PR	25-MAR-2002; 2002US-00105992.		
PR	28-AUG-2002; 2002US-00292662.		
PR	30-OCT-2002; 2002US-00284014.		
PR	30-OCT-2002; 2002US-00284059.		
PR	09-DEC-2002; 2002US-00314881.		
XX	(MILL-) MILLENNIUM PHARM INC.		
XX	Glucksmann MA, Williamson MJ, Tsai F, Rudolph-Owen LA;		
PI	Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;		
XX	WPI; 2004-090469/09.		
DR			
XX			
XX	New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413,		
PT	22438, 23553, NARC SC1 or NARC 1) useful for diagnosing, preventing or		
PT	treating disorders associated with the protein, e.g. cancer,		
PT	atherosclerosis or AIDS.		
XX			
XX	Claim 1; SEQ ID NO 39; 260pp; English.		
PS			
XX	The present invention provides isolated nucleic acid molecules and		
CC	proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SC1,		
CC	NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4,		
CC	NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20,		
CC	NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C,		

XX
PS
Claim 1: SEQ ID NO 39: 260pp: English.

xx The present invention provides isolated nucleic acid molecules and
cc proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC
cc NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC
cc NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC
cc NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 1

Db	2008 ATGATAGG 2015	
RESULT 15		
ABA09667		
ID	ABA09667 standard; DNA; 2477 BP.	
XX		
AC	ABA09667;	
XX		
DT	15-JAN-2002 (first entry)	
XX		
DE	Human bone marrow expressed oligonucleotide SEQ ID NO: 176.	
XX		
KW	Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary;	
KW	antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;	
KW	antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;	
KW	antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;	
KW	immunostimulant; analgesic; cerebroprotective; antianaemic; infection;	
KW	nervous system disorder; autoimmune disorder; inflammation; allergy; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200174836-A1.	
XX		
PD	11-OCT-2001.	
XX		
PF	30-MAR-2001; 2001WO-US010472.	
XX		
PR	31-MAR-2000; 2000US-00540217.	
XX		
PR	23-AUG-2000; 2000US-00649167.	
XX		
PR	30-NOV-2000; 2000US-0250583P.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;	
XX		
DR	WPI; 2001-626375/72.	
XX		
PT	New bone marrow-expressed nucleic acids and polypeptides, useful for	
PT	diagnosis, treatment of inflammatory, autoimmune, neurological, cancer	
PT	and increasing hematopoiesis, stem cell survival and bone growth and	
PT	remodeling.	
XX		
PS	Claim 1; Page 254-255; 380pp; English.	
XX		
CC	The present invention relates to bone marrow expressed polynucleotides	
CC	and proteins. These sequences can be used in the treatment of	
CC	inflammatory conditions (eg arthritis, Crohn's disease), cancer, central	
CC	and peripheral nervous system diseases and neuropathies, such as	
CC	Alzheimer's, Parkinson's and Huntington's diseases, spinal cord	
CC	disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid	
CC	cell disorders, platelet disorders, stem cell disorders, bone	
CC	degenerative disorders, autoimmune disorders, for example multiple	
CC	sclerosis, diabetes and arthritis, viral and bacterial infections,	
CC	allergies and blood coagulation disorders. The present sequence is a DNA	
CC	of the invention	
XX		
SQ	Sequence 2477 BP; 681 A; 500 C; 642 G; 654 T; 0 U; 0 Other;	
	Query Match 43.9%; Score 1406; DB 5; Length 2477;	
	Best Local Similarity 95.7%; Pred. No. 0;	
	Matches 1482; Conservative 0; Mismatches 0; Indels 66; Gaps 1;	
QY	616 AGGGTGAAGCTGACACTAGAGGCGCTGGAGGAGATGACGATAGGGTATCTCCCACT 675	
Db	996 AGGGTGAAGCTGACACTAGAGGCGCTGGAGGAGATGACGATAGGGTATCTCCCACT 1055	
QY	676 GTACTCCCAAAATGCTCAATAGCTTGGAGATATCTTTAATAGCGACAATGAGTTCAAG 735	
Db	1056 GTACTCCCAAAATGCTCAATAGCTTGGAGATATCTTTAATAGCGACAATGAGTTCAAG 1115	
QY	736 TGCAGGCATTCACACCGGAGTGTGGTTATGGCTTGCAGGCTGATCGTTGGACAGATAC 795	

Db	1116 TGCAGGCATTCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTAC 1175	
QY	796 AGCATACAGACGATGGAACCCAGATAACCTGGAACTAATCTTTGATTTTTCGAAGAAGAT 855	
Db	1176 AGCATACAGACGATGGAACCCAGATAACCTGGAACTAATCTTTGATTTTTCGAAGAAGAT 1235	
QY	856 CTCAGTGACACGTCAGTTTCAGGGTGATGCCCTTCTCTGGACATGTGGGTACAGCTTCTC 915	
Db	1236 CTCAGTGACACGTCAGTTTCAGGGTGATGCCCTTCTCTGGACATGTGGGTACAGCTTCTC 1295	
QY	916 TTATCATCCACATTCCTGAGAGTGAAAGAGTGTGGAAATCTTACTCTTCCCATCATG 975	
Db	1296 TTATCATCCACATTCCTGAGAGTGAAAGAGTGTGGAAATCTTACTCTTCCCATCATG 1355	
QY	976 AGCAGAAATTCGCGAAACAAATAGCAAGTGAGAGTTGACTATATAATTAATAAGCCA 1035	
Db	1356 AGCAGAAATTCGCGAAACAAATAGCAAGTGAGAGTTGACTATATAATTAATAAGCCA 1415	
QY	1036 TTACCAGGATACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATTGGAAGCCCAAGATA 1095	
Db	1416 TTACCAGGATACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATTGGAAGCCCAAGATA 1475	
QY	1096 CCATTGGATTTGGCCATCGAGTGCAGGAACTCTACAACTCCAGCTGGCTAAA 1155	
Db	1476 CCATTGGATTTGGCCATCGAGTGCAGGAACTCTACAACTCCAGCTGGCTAAA 1535	
QY	1156 GTTCAAGAAATACTATTGCTTTTAAAGAAATGCTGTAGTCATGTCGAGCCTTTGTA 1215	
Db	1536 GTTCAAGAAATACTATTGCTTTTAAAGAAATGCTGTAGTCATGTCGAGCCTTTGTA 1595	
QY	1216 GAATTTGACGTACACCTTTCAAAGGACTTTGTCCCGTGGTATATCATGATCTTACTGT 1275	
Db	1596 GAATTTGACGTACACCTTTCAAAGGACTTTGTCCCGTGGTATATCATGATCTTACTGT 1655	
QY	1276 TGTTCGACTATGAAAGAAATTTGATGCTGTGATCCAGTTTGAATTTTGAATTCAGTA 1335	
Db	1656 TGTTCGACTATGAAAGAAATTTGATGCTGTGATCCAGTTTGAATTTTGAATTCAGTA 1715	
QY	1336 AAGAATTAACATTTGACCACTCCAGTTTGTAAAGCTCACTCATGTCGACCTGAGAAA 1395	
Db	1716 AAGAATTAACATTTGACCACTCCAGTTTGTAAAGCTCACTCATGTCGACCTGAGAAA 1775	
QY	1396 TCTAAGGATCGGAAGAACTCTGTGTTTCAGAGGAAAAATTCCTTTTCAGAAAAATCAGCCA 1455	
Db	1776 TCTAAGGATCGGAAGAACTCTGTGTTTCAGAGGAAAAATTCCTTTTCAGAAAAATCAGCCA 1835	
QY	1456 TTTCTCTTCTTAAGATGTTTGTAGAGTCTTTCGCCAGAGATGTAGGGTTTAACTTGA 1515	
Db	1836 TTTCTCTTCTTAAGAT----- 1852	
QY	1516 ATAAATGGATTCGCCAGCAAGGATGGATGTGGATGGTAACTTATCAACATATTTT 1575	
Db	1853 -----GGATGGAATGTGGATGGTAACTTATCAACATATTTT 1889	
QY	1576 GACATGAATCTGTTTGGATATAATTTTAAACCTGTTTAAAGAAATTCGCGGAGAGG 1635	
Db	1890 GACATGAATCTGTTTGGATATAATTTTAAACCTGTTTAAAGAAATTCGCGGAGAGG 1949	
QY	1636 AGAATAGTGTCTTTCATTTGATGAGATATTTTGCAATGTTTCGGCAAAAGCAGAAC 1695	
Db	1950 AGAATAGTGTCTTTCATTTGATGAGATATTTTGCAATGTTTCGGCAAAAGCAGAAC 2009	
QY	1696 AAATATCCGATACCTATTTTAACTCAAGGAAAAATCTGAGATTTATCTGAACTCATGGAC 1755	
Db	2010 AAATATCCGATACCTATTTTAACTCAAGGAAAAATCTGAGATTTATCTGAACTCATGGAC 2069	
QY	1756 CTCAGATCTCGGACCAACCCCATTTGCAAGCTTTGCAAGTTTGAATCTTACTGGGG 1815	
Db	2070 CTCAGATCTCGGACCAACCCCATTTGCAAGCTTTGCAAGTTTGAATCTTACTGGGG 2129	
QY	1816 ATAAATGTACATCTGAAAGACTTGTCCAGAAACCCATCCTATATTCAAGAGGCAAAAGCT 1875	
Db	2130 ATAAATGTACATCTGAAAGACTTGTCCAGAAACCCATCCTATATTCAAGAGGCAAAAGCT 2189	


```
Qy 1876 AAGGACTAGTCATATTCCTGGGGTGATGATACCAATGATCCTGAAACACAGAGGAAA 1935
Db |||||
Qy 2190 AAGGACTAGTCATATTCCTGGGGTGATGATACCAATGATCCTGAAACACAGAGGAAA 2249
Db |||||
Qy 1936 TTGAAGGAACTTGGAGTTAAATGCTCTAATTTATGATAGGATATATGATTGGATGCTGAA 1995
Db |||||
Qy 2250 TTGAAGGAACTTGGAGTTAAATGCTCTAATTTATGATAGGATATATGATTGGATGCTGAA 2309
Db |||||
Qy 1996 CAACCAATATATCCAAAGTGGAGCAATTGGAAACGCTGAACAGGAAATTGCCAGAGCTT 2055
Db |||||
Qy 2310 CAACCAATATATCCAAAGTGGAGCAATTGGAAACGCTGAACAGGAAATTGCCAGAGCTT 2369
Db |||||
Qy 2056 AAGAGCTGTTGTGTCCCACTGTTAGCCGCTTGTTCCTCATCTTTGTGTGGGAGTCT 2115
Db |||||
Qy 2370 AAGAGCTGTTGTGTCCCACTGTTAGCCGCTTGTTCCTCATCTTTGTGTGGGAGTCT 2429
Db |||||
Qy 2116 GATATCCATGTGGATGCCAACGGCATTGATAACGTGGAGAAATGCTTAG 2163
Db |||||
Qy 2430 GATATCCATGTGGATGCCAACGGCATTGATAACGTGGAGAAATGCTTAG 2477
Db |||||
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Search completed: July 2, 2005, 13:08:15
Job time : 1645 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2005, 12:40:51 ; Search time 9973 Seconds
(without alignments)
12236.443 Million cell updates/sec

Title: US-10-047-855-4
Perfect score: 3206
Sequence: 1 gtcgaccacgcgtccggc.....aaaaaaagcgccgcg 3206

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2038	63.6	3142	3	AK030645 Mus muscu
2	2032	63.4	3614	3	AK050318 Mus muscu
3	1891	58.7	3248	3	BC006887 Mus muscu
4	1794.6	56.0	3578	3	AK031658 Mus muscu
5	1570.6	49.0	2604	3	AK009563 Mus muscu
6	1420.2	44.3	2228	3	AK051728 Mus muscu
7	1170.8	36.5	1618	3	AK049491 Mus muscu
8	962.6	30.0	998	5	EX344122 BX344122
9	921.4	28.7	1006	5	EX344123 BX344123
10	846.8	26.4	882	4	BM457674 AGENCOURT
11	835	26.0	1128	4	BM478430 AGENCOURT
12	816	25.5	973	5	BQ049943 AGENCOURT
13	815.2	25.4	948	5	BUI45581 AGENCOURT
14	809.4	25.2	811	3	CR623938 full-leng
15	799.8	24.9	811	5	AL520917 AL520917
16	758.6	23.7	818	5	BX403389 BX403389
17	749.2	23.4	758	6	CD520772 AGENCOURT
18	746.8	23.3	786	1	AL520916 AL520916
19	739.2	23.1	823	1	AL046038 DKFZp434B
20	731.4	22.8	754	7	CN303372 170006000
21	728.2	22.7	776	4	BG742916 602632004
22	722.2	22.5	735	7	CR768972 DKFZp468H
23	706.8	22.0	855	5	BQ962080 AGENCOURT
24	699.8	21.8	821	4	BI822275 603036411

25	697	21.7	783	6	CD466056 LeukoN2.1
26	692.8	21.6	696	2	AW327746 dr01g04.x
27	687	21.4	711	5	BX507382 DKFZp779K
28	686.4	21.4	688	4	BM786845 K-EST0065
29	681	21.2	731	6	CB310051 AGENCOURT
30	670.4	20.9	795	4	BG623187 602648092
31	658	20.5	672	5	EX091262 EX091262
32	653.4	20.4	728	7	CN303370 170004243
33	644.2	20.1	746	7	CN303375 170005318
34	635.8	19.8	833	4	BI144681 602909978
35	633.4	19.8	768	1	AUI136888 AUI136888
36	632	19.7	901	6	CB196769 AGENCOURT
37	631.2	19.7	805	6	CA317224 UI-M-FWO-
38	627.6	19.6	958	5	BUS03488 AGENCOURT
39	623	19.4	691	7	CK833283 4057562 B
40	620	19.3	656	7	CK001576 AGENCOURT
41	616	19.2	619	5	BQ002886 UI-H-E11-
42	614.2	19.2	654	4	BI838003 603083846
43	608.8	19.0	841	1	AJ820056 AJ820056
44	608.8	19.0	656	4	BI561344 603255105
45	603.8	18.8	665	6	CD640091 AGENCOURT

ALIGNMENTS

RESULT 1	AK030645	3142 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK030645	3142 bp	mRNA	linear	HTC 03-APR-2004
DEFINITION	Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430401018 product:hypothetical Glyceraldehyde-3-phosphate dehydrogenase/Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.				
ACCESSION	AK030645				
VERSION	AK030645.1	GI:26326638			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipette sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
REFERENCE	5				

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3142)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: <http://genome.gsc.riken.jp/> URL: <http://fantom.gsc.riken.jp/> Location/Qualifiers

FEATURES

source 1..3142 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:5430401018" /db_xref="taxon:10090" /clone="5430401018" /tissue_type="head" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="6 days neonate" 157..2184

CDS /note="unnamed protein product: hypothetical Glycerophosphoryl diester phosphodiesterase(Glycosyl hydrolase, starch-binding domain containing protein (InterPro|IPR004129, InterPro|IPR002044, evidence: InterPro) putative" /codon_start=1 /protein_id="BAC27063.1" /db_xref="GI:26326639" /translation="MTPSQVTFEIRGTLLPGVEFAICGSDALGNWNPQNAVALIN ETGDSLVKAVIALNRGVSVKVRPRGCFLEPKTIGPCQVIVHKWETHLPQPSITPL ESEIIDDQGIHNGVETLDSGLTCTQTEIRLRLHSEKPPVSIKKPKSPRVK LTLGLEDEDDDDKVSFTVLHMKNSLEISLSDNFEKCRHSGQPEGCGYLGQPDRT EYSQTMEFDNLELFDVFEEDLSEHVVGQDVLFGHVFTACLSTLSAERSAGILT LPINRSNRKTIKVRVDFIIKPLPGYSCMSQSFYSKYWPRIPLDVGHRGAGNST TAKLAKVQENTIASRNAASHGAAPFVDFVHLSKDFVPVYVHDLTLCILTKMRKYEAD VELPPIPVKLTFDQILLKLSHVLTAKDKRKOSLYEENFFSENQFPPLKRWLVLS LPENVGFNLEIKWICQHRDGYWDCNLSYFDNVPFLDILILKTVLENSKRRIVSSPD ADICTWVRQKNQYPIELFELTQKSDIYFELMDLRSRTPPIAMSAFQENILGINAHTE DLLRNPSYVQAKAGLVIFCWGDDTNDPNRKLKFEVGNGLIYDRIVWMPQPNL FQVEQLERLKOELPBLKNCLEPTVSHFIPSSFCVEPDIHVDANGIDSVENA" 3125..3130

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Best Local Similarity 82.9%; Pred. No. 0;
Matches 2579; Conservative 0; Mismatches 450; Indels 81; Gaps 19;

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DB 98 GCCGCGCCGAGGCTCTCGCGCGCGCGCGGAGCGGAGAAATCCTAAAAATTCATCAGAA 157

QY 146 TGACACCTTCTCAGGTGCTTTTGAATAAGAGGAAGTCTTTTACCAGAGAGATTTTTCG 205
DB 158 TGACACCTTCTCAGGTGCTTTTGAATAAGAGGAAGTCTTTTACCAGAGAGATTTTTCG 217

QY 206 CGATATGTGGAAGCTGTGATGCTTTGGGAACTTGGGAATCTCTCAAAATGCTGTGGCTCTTC 265
DB 218 CAATATGTGGAAGCTGTGATGCTTGGGAACTTGGGAATCTCTCAAAATGCTGTGGCTCTTC 277

QY 266 TTCACGAGATGACACAGAGTGAAGCATGCTATGGAAGCAACCATTTGTACTCAGTAGAG 325
DB 278 TTAATGAACGAGACAGGAGACAGTGTGTTGGAAAGCAGTGATTTGCTCTCAATAGAG 337

QY 326 GAGTATCAGTTCAGTTCGCTACTTCAAAGGGTACTTTTGTAGAACCAAGACTATCGGTG 385
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QY 386 GTCATGTCAAGTGAAGTGTTCACAAGTGGGAGACTCATCTACCAACCAAGCATCAATAACCC 445
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QY 626 TGACACTAGAAAGCTGGAGGAAGATGACGAT-----GATAGGGTATCTCCCACTG 676
DB 638 TCACACTGAGGGTCTGGAGGAAGATGAAGATGATGATGACGATAGGTCTCTCCCACTG 697

QY 677 TACTCCACAAAATGTCCAATAGCTTGAGATATCTTTAATAAGGCAATAGATTGATCTAAGT 736
DB 698 TTCTTCCAAAATGTCCAAGCTGAGATATCTTTAATAAGTGAATAGATTGATCTAAGT 757

QY 737 GCAGGCATTCACAGCGGAGTGTGGTTATGGCTTGAGCTGATCGTTGGACAGAGATACA 796
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DB 818 GCATACAGACAAATGGAAACAGATAAATCTGGAGCTCATCTTTTGATCTTTTGTAGGAAGATC 877

QY 857 TCAGTGAGCAGTAGTTTCAGGGTATGCCCTCTCTCGACATGTGGGTACAGCTTGTCTCT 916
DB 878 TCAGTGAGCATGTAGTTTCAGGGTATGTTCTTCTCGACACGTTGGGACAGCATGCTCCTC 937

QY 917 TATCATCCACATTGCTGAGAGTGGAAAGAGTGTCTGGAATCTTACTCTTCCCATCATGA 976
DB 938 TGTCTTCTACCATTCGCTGAGAGTGGAAAGAGCGCTGGAATCCTTACTCTTCCCATCATGA 997

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DB 998 GCAGAAATTTCCAGAAACCAATAGGCAAGTGTAGAGTTGATTTTATCATCATCAAGCCAT 1057

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DB 1058 TACCTGGATATAGTTGTTCTTATGCAGTCTTCAITTTTCCAAAGTATTTGGAACCAAGATAC 1117

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[illegible]

Db	2198	GAGGACATTTAGGGGACACCGCTGCCCTCATG-----TTTAGTTTTTCCCATCGAGCACT	22553
Qy	2237	GTTGATCTATGCGCTTTTGGGCTTCTCAGTTTCAATGAAGCAATAATGAAGTATTTAACTCT	2296
Db	2254	GCTG----TTGGCTCTTAGGTTTTTTCAGTCCCATGAAGCAATAATGAAGTATTTTACTAT	2309
Qy	2297	TTCACTACAGTCTTTGCAAGTATGCTA-----TTTAAATTTACTTTGGCCAGGTATATAATT	2349
Db	2310	TTCAATACAGGTCCTGCGCAAGAAATATCAAGTATGCTATTGTGCTACTTCTCCAGGTATATAATT	2369
Qy	2350	GCCAGTCAGTCTCTTTATAGTGTGAAATTTATTTGGTTAGTAAATATAAATATTTTAAACT	2409
Db	2370	ACCAATCAGTCTCTGTACAATAAGAAATATACGT-----TTTAAATTTTCAGTG	2419
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Db	2468	ACGATATAAATATCTCATCTCTAAAGTTCAGGCTTTTTCATTTGATTAAGTCTTAAATCTT	2527
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Db	2528	CAGTCTTGAGAAAAATGA---TTGCTAATTTATACCTGACCATGGAATACTAAGTACCT	2585
Qy	2590	CAATGCATGCATTTTGCACTGGTGATTTCCAACCTGCACAAATCTTTGTGCCACTTTGTATA	2649
Db	2586	C-AATGCATGCATTTTGCACTGGTGGCTCCAGCTGCACAGTCTGTGT-CATCCATGTACA	2643
Qy	2650	TAGTATTTTTTACATGGTTTGCATGCAACACACCACTTTTCATTTCAGTATGAACCTT	2709
Db	2644	TAGGTATCTTTT--ACATGGTTTGTAGGAACAC--GCACCATTTTTCCTTTAGTATAAACCC-T	2699
Qy	2710	GAGGCTCTGCATTTTTCACCTTTTAAACCAACAGCCCTGAAGGTGAACCTTCGAAACTTGT	2769
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Qy	2770	TTCATAAATCTTTCAAAGTTGTTTTACATCAATGTTTAAAAATTTCAAATGCTGCAGGGT	2829
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Qy	2950	TTACTGTTAGTCTCTGCATCTGTGGTGTGCTAGGTAGTATGAGAAGATGTCAGGACTGG	3009
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Qy	3010	ACGTATTTTTTGTGCTTAAAAAAGGCTGTTTGTAGGCGTTTAAATATGCTTATTTT	3069
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RESULT 2	
AK050318	
LOCUS	
DEFINITION	

starch-binding domain containing protein, full insert sequence.
AK050318
VERSION AK050318.1 GI:26093898
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

6
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>

FEATURES

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polyA_site

ORIGIN

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Matches 2584; Conservative 0; Mismatches 450; Indels 82; Gaps 20;
QY 86 GAGCGGACCTCGGACTAGCGAACCGGAGCAGCATCAATAAATAAATCCATCAGAA 145
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QY 146 TGACACCTTCTCAGGTTCCTTTGAATAAGAGGAACTCTTTTACCAGGAGAGGTTTTC 205
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QY 266 TTCAGAGATGACACAGGTGAAGCAGTCTATGGAAGCAACCATTTGTTACTCAGTAGAG 325
Db 238 TTAATGAAACGACAGCAGGAGCAGTGTTGTGGAAAGCAGTGATTCCTCAATAGAG 297
QY 326 GAGTATCAGTTCAGTATCGCTACTCTCAAGGGTACTTTTGAACCAAGAGACTATCGGTG 385
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QY 386 GTCCATCTCAAGTGATAGTTTCAAGTGGAGACTCAATCTACAAACGATCAATAACC- 444
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QY 505 ACTCTGATTTCTGATGGCTGACATGTGACATGCAATTAAGATTTACGTTTGCATTTCT 564
Db 478 ACCTGATTTCTGATGGCTTACATGTCAGATGAATATAGATTCGCTGCAATTTCT 537
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QY 625 CTGACACTAGAGGCTGGAGGAAGATGACGAT-----GATAGGTTATCTCCCACT 675

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RESULT 3			
BC006887		3248 bp mRNA linear HTC 19-NOV-2003	
LOCUS	Mus musculus RIKEN CDNA 2310032D16 gene, mRNA (CDNA clone IMAGE:3596618), containing frame-shift errors.		
ACCESSION	BC006887		
KEYWORDS	HTC.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3248)		
AUTHORS	Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wexler, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Smalls, D.E., Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
JOURNAL	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	22388257		
REFERENCE	12477932		
AUTHORS	2 (bases 1 to 3248) Straussberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabs@remail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc.		

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[illegible]

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RESULT 5			
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DEFINITION		Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032D16 product:hypothetical Glycero-phosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.	
ACCESSION		AK009563	
VERSION		AK009563.1 GI:12844432	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
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JOURNAL		Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE		99279253	
PUBMED		10349636	
2		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
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ORIGIN

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Query Match 49.0%; Score 1570.6; DB 3; Length 2604;
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Matches 2041; Conservative 0; Mismatches 364; Indels 72; Gaps 18;

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QY 895 CATGGGGTACAGCTTGTCTTATCATCCACCATGCTGAGAGTGGAAAGAGTGTCTGGA 954
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ORIGIN

Query Match 44.3%; Score 1420.2; DB 3; Length 2228;
Best Local Similarity 81.9%; Pred. No. 0;
Matches 1878; Conservative 0; Mismatches 343; Indels 72; Gaps 18;
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DB 1141 CAAAGTGGAGCAGTTTGGAGCGCTGAAAGCAAGAAATTCGAGAGCTTTAAGAACTGTTGTGT 1200
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DB 1201 CCCACTGTAGCGCTTTGTTCCCTCATCTTTGTTGGGGAGTCTGATATCCACGTTGAT 1260
QY 2131 GCCAAGCAGCAATTTGAAAGTGGAGAACTGTAGTTTATTTGACAGAGGTCATTTTGGG 2190
DB 1261 GCCAAGCAGCAATTTGATGTTGGAGAACGCTTAGTTTCAAGTGCACAGAGGACATTTAGGG 1320
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DB 1321 GCACACCGCTGCGCTCATG---TTTAGTTTTCACCATCGAGCACTGCTG---TTGCT 1372
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DB 1373 CTTAGTTTTCAGTCCCAATGAAGCAATAATGAAGTATTTTACTATTTTCACTACAGTTCT 1432
QY 2311 TGCAAGTATGCTATTTTAAAT---ACTTGGCCAGGTATAATTTGCCAGTCACTCT 2363
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QY 2424 ATAATGTTAAACATATGTTTCAATTAAGCATGACCTTTGAAATTTAACTATATAAATAGC 2483
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QY 2544 AATGACTATGATATTAATATACCTGACCAATGAAATAAATAAGTACCTCAAAATGCATGCAAT 2603
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QY 2604 TGCATGTTGATTTCAACTGACAAAATCTTTGTGGCCATCTTGTATATAGGATTTTGTAC 2663
DB 1708 TGCATGTTGGCTCCAGCTGACAGCTCTGTGT---CATCCATGTACATAGGTATCTTT---A 1764
QY 2664 ATGGTTTCACTGACACAAACCACTTTTCACTTCACTAGTATGAACCTTTGAGGCTGCTGCCAT 2723
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Qy	2724	TTTTCCACTTAACCAACGAGCTGAAGGTGAACCTCGAAACTTGTGTTTCATAAAATCTTTC	2783
Db	1823	TTCTCACTGACCCAGCAGCCCTGCAGATGAACCTCAAACTTGTCTCATPAACCAATTC	1882
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Db	1883	AAA-----GATATTAAAGTTCAGAAATGCTGCAGGGTAATTTAATGTATAA	1928
Qy	2844	AATATTAGTAAGAAAAGTATTGTCATCTTAGTCATCTTAGTAGTAGAATAGATACACATCAAAAT	2903
Db	1929	AGTATTGTTAAG--AAGTATATATTGCATATATAGTAGTAGTGTAGATCAGAAGGTATCAAT	1985
Qy	2904	TCAATTCACTGCATGCTTTAGTGTTAAGCATGATGATGTACATGTTTACGTGTTAGTGCC	2963
Db	1986	TTGACTCAATGCATGCTTTAGGTTTTAAGCAAGATGTTACATGTTTACTGTTAAGTGCC	2045
Qy	2964	TTGCATCTGTGCTGTAGTGTAGTATGAGAAGATGTCGAAGACTGGACGTATTTTGTTCG	3023
Db	2046	TTGCATC--TGGTCTAGTTCAG-----GGAGATGTTAAGGACATAAATATTTTGTTCG	2098
Qy	3024	CTAAAAAAAAGGCTGTTTGTAGCGGTTTTAAATATGCTTATTTTGTGTCTCTCACT	3083
Db	2099	CTAAAAAACAAGTCTGTTT-TAGACACTTTGAGTATGCTTATTTAGTGTCTCACTACCT	2157
Qy	3084	ACCTATTACACACTGTGCTTTGTGGTGTGTTTGTATGTCGTGCTTATATACAGTAGT	3143
Db	2158	AGTAAACAATAGTGTCTCACTACCCAGTAAACAT--AATTGCTGTGTGTCATAGTAGT	2215
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Db	2216	TAAATTTCCATGC	2228
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AK049491			
LOCUS	1618 bp	mRNA	linear
DEFINITION	Mus musculus 7 days embryo whole body cDNA, RIKEN full-length	HTC 03-APR-2004	
	enriched library, clone:C430017C03 product:hypothetical		
	Glycerophosphoryl diester phosphodiesterase/Glycosyl hydrolase,		
	starch-binding domain containing protein, full insert sequence.		
ACCESSION	AK049491		
VERSION	AK049491.1	GI:26340223	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1		
AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,		
	Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagao,K., Sasaki,N., Carninci,P.,		
	Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,		
	Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,		
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	Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,		
	Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,		
	Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format		
	sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		

11076861			
4			
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the		
AUTHORS	FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409, 685-690 (2001)		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research		
	Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation		
JOURNAL	of 60,770 full-length cDNAs		
REFERENCE	Nature 420, 563-573 (2002)		
AUTHORS	6 (bases 1 to 1618)		
	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,		
	Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,		
	Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,		
	Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,		
	Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,		
	Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,		
	Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,		
	Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N.,		
	Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,		
	Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,		
	Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,		
	Muramatsu,M. and Hayashizaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of		
	Physical and Chemical Research (RIKEN), Laboratory for Genome		
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),		
	RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,		
	Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,		
	URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,		
	Fax:81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome		
	Encyclopedia Project of Genome Exploration Research Group in Riken		
	Genomic Sciences Center and Genome Science Laboratory in RIKEN		
	Division of Experimental Animal Research in Riken contributed to		
	prepare mouse tissues.		
	Please visit our web site for further details.		
	URL:http://genome.gsc.riken.jp/		
	URL:http://fantom.gsc.riken.jp/		
FEATURES	Location/Qualifiers		
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	/strain="C57BL/6J"		
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	/db_xref="taxon:10090"		
	/clone="C430017C03"		
	/tissue_type="whole body"		
	/clone_lib="RIKEN full-length enriched mouse cDNA library"		
	/dev_stage="7 days embryo"		
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	VHGRAGNSTTTAKLVQENTIASLRNAASHGAFFVDFVHLSKDFVPVYHDLTCC		
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	PFPLKWLSELPENGFNIQIKWICQHRDVGWGNLSTYFDMNVFLDIILKTVSQNS		
	GNRIYVFSFDADICTMRVQKQNPILFTQKSDIYPELMDLRKRTTPIAWSFQAF		
	ENRILNATDEDLIRNPVYQEAQKGLVFCWDDTNDPERRKLKEFGVGLIYDR		
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	VENA"		
ORIGIN			
Query Match	36.5%;	Score 1170.8;	DB 3; Length 1618;

Best Local Similarity 84.1%; Pred. No. 7.6e-261; Matches 1361; Conservative 0; Mismatches 242; Indels 15; Gaps 3;	
QY 845	TCGAAGAAGATCTCAGTGACACAGTAGTTCAGGGTGATGCCCTTCTCTGACATGTGGGTA 904
Db 1	TTGAGGAAGATCTCAGTGACACAGTAGTTCAGGGTGATGTTCTCTGACAGTGGCA 60
QY 905	CAGCTGTCTCTTATCATCATCAGTGTGAGAGTGGAAGAGTGTGGAATCTTACTC 964
Db 61	CAGCATGCCCTCTCTCTTCTTACCATTTGCTGAGAGTGGGAAGCGCTGGAATCTTACTC 120
QY 965	TTCCCATCATGACAGCAAAATTCCTCCGGAACAAATAGCAAGTGAGAGTTGACTATAA 1024
Db 121	TTCCCATCATGACAGCAAAATTCAGAAAACAACTATAGCAAGTGCAGAGTTGATTTATCA 180
QY 1025	TTATTAAGCCATTAACCAAGGATACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATGGA 1084
Db 181	TCATCAAGCCATTAACCTGGGATATAGTTGTTCTATGCACTTTCATTTTCCAAAGTATGGA 240
QY 1085	AGCCAGAATACCATTTGGATGTTGGCGATCGAGTGCAGGAACCTCTCAACAACTGCC 1144
Db 241	AACCAAGAATACCATTTGGAGTGTGGACATCGTGTGCGAGGAACCTCAACAACTGCCA 300
QY 1145	AGCTGGCTAAAGTTCAGAAATACTATTGCTTCTTTAAAGAACTGCTAGTCATGGTG 1204
Db 301	AGCTAGCTAAAGTACAGGAATACTATGCTTCTTTAAAGAACTGCTGCGAGTCAATGGCG 360
QY 1205	CAGCTTTGTAGAAATTTGACGTACACCTTTCAAGGACCTTTGCGCCGTTGATATCATG 1264
Db 361	CAGCAATTTGTAGAAATTTGATGTCACCTTTCAAGGACCTTTGCGCCGTTGATATCATG 420
QY 1265	ATCTTACTGTTGTTGATGATGAAAGAAATTTGATGCTGATCAGTTGGAATTTTG 1324
Db 421	ACCTCACCTGCTGCTGACCATGAAGAGGAAATATGAAGCTGATCAGTTGAATTTTG 480
QY 1325	AAATCCAGTAAAGAAATTAACATTTGACCACTCCAGTTGTTAAAGCTCACTCATGCA 1384
Db 481	AAATCCAGTAAAGAAATTAACATTTGACCACTCCAGTTGTTAAAGCTTCTCATGCA 540
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Db 541	CTGCATTAACCAAGACCGGAAACAACTTTGTTATGAGGAGGAAATCTTTTCTG 600
QY 1445	AAATCAGCAATTCCTCTCTTAAAGATGTTTGTAGAGTCTTTGCGAAGATGTAGGT 1504
Db 601	AAATCAGCAATTCCTCTCTTAAAGATGTTTGTAGAGTCAATTCGCAAGAAATGTAGAT 660
QY 1505	TTAACATTTGAAATTAAGATCTGCGACCAAGGATGGAATGCGGATGTAATTTAT 1564
Db 661	TTAATATACAAATAAATGGAATTTGCCAACACAGGATGGAGTATGGGATGGCACTTAT 720
QY 1565	CAACATATTTGACATGAATCTGTTTTCGATATATTTTAAAGAACTGTTTGTAGAAAT 1624
Db 721	CAACATATTTGATATGAATGTTTTCGATATATTTTAAAGAACTGTTTGTAGAAAT 780
QY 1625	CTGGGAAGAGGAGATAGTGTCTTCTTCAATTTGATGACATATTTGCAAAATGTTTCGC 1684
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QY 1685	AAAGCAGAACAAATATCCGATATTTTAACTCAAGGAAATCTGAGATTTATCTCTG 1744
Db 841	AGAAGCAGAACAAATATCCCATATTTTGTGACCAAGGAAATCTGATATTTACCCCG 900
QY 1745	AATCATGACCTCAGATCTCGGACAAACCCCAATTCGATGAGTTTTCGACAGTTTGA 1804
Db 901	AATCATGACCTCAGATCTCGGACAAACCCCAATTCGATGAGTTTTCGACAGTTTGA 960
QY 1805	ATCTACTGGGGATAAATGTATCACTAGAGACTTGTCTGAAACCCCACTCTATATTCAG 1864
Db 961	ATATTTGGGGATAAATGTATCACTAGAGACTTGTCTGAAACCCCACTCTATATTCAG 1020
QY 1865	AGCAAAAGCTAAGGAGTATGATATTTCTGCTGGGATGATGATCAATGATCTCTGAA 1924
Db 1021	AGCAAAAGCTAAGGATGATGATATTTCTGCTGGGATGATGATCAATGATCTCTGAA 1080
QY 1925	ACAGAAGGAAATTTGAAGAACTTTGAGTTAAATGCTCTAAATTTATGATGATATATGAT 1984
Db 1081	ACAGAAGGAAATTTGAAGAAATTTGAGTTAAATGCTCTAAATTTATGATGATATATGAT 1140
QY 1985	GGATCCCTGGAACAAACAAATATATTTCCAAGTGGAGCAATTTGGAACGCTGGAAGCAAT 2044
Db 1141	GGATCCCTGGAACAGCAAAATATATTTCCAAGTGGAGCAATTTGGAAGCGCTGGAAGCAAT 1200
QY 2045	TCCCAGAGCTTAAGAGCTGTTTGTGCTCCACATGTTAGCGCTTGTTCCTCTCATCTTCT 2104
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QY 2105	GTGGGAGTCTGATATCCATGTGATGCAACCGCAATTTGATAACGCTGGAGATGCTTAT 2164
Db 1261	GTGTGGAGCTGATATCCAGTGGATGCAACCGCAATTTGATAGTGTGGAGAACGCTTAT 1320
QY 2165	TTTTATTGCAAGAGTCAATTTTGGGGGGTGCACCGCTGTTCTGGGTATTCATTTTCA 2224
Db 1321	TCACAGTGCACAGAGCAATTTTGGGGGGTGCACCGCTGCTCATG-----TTTAGTTTCA 1376
QY 2225	TCACAGTGCATGTTGATCTATGCTTCTTGGGCTTCTCAGTTCAATGAAGCAATTAAGAA 2284
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QY 2285	GTATTTAACTCTTTTCACTACAGTCTCTGCAAGTATGCTA-----TTTAAATTAATCTGG 2337
Db 1433	GTATTTTAACTCTTTTCACTACAGTCTCTGCAAGTATGCTA-----TTTAAATTAATCTGG 1492
QY 2338	CAAGTATAATTTGCAAGTCACTCTTTTATAGTGAGAAATTTATTTGTTAGTATATAA 2397
Db 1493	CCAGGTATAATTTACCAATCAGTCTCTGTACATAAGAAATATCTGTTAAACATTTCA 1552
QY 2398	ATATTTAACTAAATATATAATCTATAATGTTAAACATATGTTTCATTAAGGATA 2455
Db 1553	TGAGATATCTAAGCCTATAATGTTGAATCTTCAITAAAGTTGGAATTAACGATATA 1610
RESULT 8	
BX344122/c	
LOCUS	BX344122 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION	clone CS01059YA01 3-PRIME, mRNA sequence.
ACCESSION	BX344122
VERSION	BX344122.2 GI:46262755
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 1, 2003 this sequence version replaced gi:30309075. Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen. This sequence belongs to sequence cluster 9838.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?c=CS1A1015ZE01NP1&c=9838.r.
FEATURES	
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1..998	
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ORIGIN									
Query Match 30.0%; Score 962.6; DB 5; Length 998;									
Best Local Similarity 96.7%; Pred. No. 1.7e-212;									
Matches 965; Conservative 14; Mismatches 19; Indels 0; Gaps 0;									
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Qy	2268	AATGAAGCAATAA	TCAAGTATTTAACTCT	TTTTCACTACAGT	TTCTTGGCAAGTATG	CTATTTA	2327		
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Qy	2328	AATTACTTTGGCCAGGT	ATAATGTC	CAGTCTCTTTATAGT	GAGAAAAATTTAT	TTCGGT	2387		
Db	818	AATTACTTTGGCCAGGT	ATAATGTC	CAGTCTCTTTATAGT	GAGAAAAATTTAT	TTCGGT	759		
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Qy	2688	ATTTTCATT	CAGTATGAACCTT	GAGGCTGCGCCAT	TTTTTCCACTTAAC	CCAAAC	2747		
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Qy	2748	GAAGGTGAAC	CTCGAAACTCTG	TTTCATAAACTCT	TTTCAAAAGTGT	TTTTTACATCAAT	2807		
Db	398	GAAGGTGAAC	CTCGAAACTCTG	TTTCATAAACTCT	TTTCAAAAGTGT	TTTTTACATCAAT	339		
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ACCESSION	3145			
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TITLE	3145			
JOURNAL	3145			
COMMENT	3145			
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Matches	950	Conservative	8	Mismatches 19; Indels 2; Gaps 2;
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Qy	1264	GATCTTACCTGTTGTTTGACTATGAAAGAAATTTGATCTGATCCAGTTGAATTTT	1323	
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Qy	1324	GAAATCCAGTAAAGAAATTAACATTTTGACCACTCCAGTTGTTTAAAGCTCACCTCATGTG	1383	
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Qy	1384	ACTGCACCTGAAATCTAAGGATCGGAAAGAAATCTGTGTTCCAGGAGGAAATTCCTTTTCA	1443	


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QY 2128 GATGCCAACGGCATATGATACGTCGAGAAATGCTTAGTCTTTTATTTGACACAGAGTCATTTT 2187
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|||
Db 781 GGGGGCGTCGACCCGCTGTCCTGGGTATTCATTTTTCATCTCATCTGAGCATTTGTCATCTATG 840
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QY 2248 CC-TTTTGGGCTTCTCAG-TTCAATGAAGCAATAA 2280
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Db 841 CTTTTTGGGCTTCTCAGTTTCAATGAAGCCATAA 875
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RESULT 11
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LOCUS AGENCOURT_6508010 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5578502
DEFINITION 5', mRNA sequence.
ACCESSION BM478430
VERSION BM478430.1 GI:18527472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1128)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.G.E. Consortium (LLNL)
Clone Distribution: MGC Clone Distribution Information can be
found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12333 row: k column: 15
High quality sequence stop: 618.
Location/Qualifiers
1. 1128
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5578502"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

FEATURES
source
Query Match 26.0%; Score 835; DB 4; Length 1128;
Best Local Similarity 91.6%; Pred. No. 7.8e-183;
Matches 1008; Conservative 0; Mismatches 71; Indels 21; Gaps 11;

QY 803 AGACGATGGAACACAGATAACCTGGAACTAATCTTTGATTTTTCGAGAAAGATCTCAGTG 862
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Db 13 AGACGATGGAACACAGATAACCTGGAACTAATCTTTGATTTTTCGAGAAAGATCTCAGTG 72
|||

QY 863 AGACGATGTCAGGTGATGCCCTTCTCGGACATGTCGTCAGTCTCTCTATCAT 922
|||
Db 73 AGACGATGTCAGGTGATGCCCTTCTCGGACATGTCGTCAGTCTCTCTATCAT 132
|||

QY 923 CCACCATGTCGAGTGGAAAGAGTGCCTGGAATTCCTTCTTCCCATCATGAGCAGAA 982
|||
Db 133 CCACCATGTCGAGTGGAAAGAGTGCCTGGAATTCCTTCTTCCCATCATGAGCAGAA 192
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QY 983 ATTCCCGGAAACAATAGGCAAGTGGAGTTGACTATATAATTAAGCCATTACCGAG 1042
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Db 193 ATTCCCGGAAACAATAGGCAAGTGGAGTTGACTATATAATTAAGCCATTACCGAG 252
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QY 1043 GATACAGTTGTGACATGAATCTTTCATTTTCCAGTATTGGAAGCAAGAATACCATTTGG 1102
|||
Db 253 GATACAGTTGTGACATGAATCTTTCATTTTCCAGTATTGGAAGCAAGAATACCATTTGG 312
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QY 1103 ATGTTGGCCATCGAGTGCAGGAAACTCTACAACTGCCAGCTGGCTAAAGTTCAAG 1162
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Db 313 ATGTTGGCCATCGAGTGCAGGAAACTCTACAACTGCCAGCTGGCTAAAGTTCAAG 372
|||
QY 1163 AAAATACTATATGCTCTTTTAAAGAAATGCTGTAGTCATGTCAGCGCTTTGTAGAAATTG 1222
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Db 373 AAAATACTATATGCTCTTTTAAAGAAATGCTGTAGTCATGTCAGCGCTTTGTAGAAATTG 432
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QY 1223 AGTACACCTTTCAAAGGACTTTTGGCCGTCGTATATCATGATCTTACCTGTGTTGA 1282
|||
Db 433 AGTACACCTTTCAAAGGACTTTTGGCCGTCGTATATCATGATCTTACCTGTGTTGA 492
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QY 1283 CTATGAAAAGAAATTTGATGCTGATCCAGTTTGAATTTTGAATAATCCAGTAAAGAAAT 1342
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Db 493 CTATGAAAAGAAATTTGATGCTGATCCAGTTTGAATTTTGAATAATCCAGTAAAGAAAT 552
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Db 553 TAACATTTGACCAACTCCAGTTTGTAAAGCTCACTCATGTCAGTGCAGTCAATCTAAGG 612
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|||
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Db 793 TGAATCTGTTTTTGGATATTAATTTTAAAACTGTTTGTAGAAATTTCTGGGGAGAGGAGA 852
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QY 1637 GAATAGTGTCTTCTCATTTTGTGATGAGATATTTTGACAA--TGGTTCCGGCAAAAGCAGAA 1694
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Db 853 AAAAAGTGTCTTCTCATTTTGTGATGAGATATTTTGGCCACTGGGTTCCGCAAGCCGAAA 912
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QY 1695 CAAATATCC---GATACTATTTTAACTCAAGGAAATCTG-AGATTATCTCTGAACTC- 1749
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QY 1750 -ATGGACCTCAGATCTCGGCAACCCCATTTGCAATGAGCTTTGCACAGTTTGAATATCT 1808
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Db 973 ATGGAATCTCAGAACTCGGACAAACCCCATTTGCAATGAGCTTTTGGCCGCTTTGAAAT 1932
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QY 1809 AC----TGGGGATAAATGTATACATAC--TGAAGACTTGTCTCAGAAA-CCCATCTATATTC 1861
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Db 1033 TCCACTGGGGATAAAGGTACCTACCTGGGAGAACTTGTCTCAAAACCCCTTCCCAATTTTC 1092
|||
QY 1862 AAGAGGCAAAAGCTAAAGGGA 1881
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Db 1093 AAAAGGCAAAAGCTAAAGGA 1112
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RESULT 12
BM049943
LOCUS AGENCOURT_7048600 NIH_MGC_85 Homo sapiens linear EST 29-MAR-2002
DEFINITION 5', mRNA sequence.
ACCESSION BM049943
VERSION BM049943.1 GI:19809283
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORIGIN

Best Local Similarity 96.6%; Pred. No. 3e-178; Matches 887; Conservative 0; Mismatches 23; Indels 8; Gaps 5;	
Qy	1430 AAAATTCCTTTTCAGAAAATCAGCCATTTCTTCTTAAGATGTTTATAGAGCTTTTGC 1489
Db	1 AAAATTCCTTTTCAGAAAATCAGCCATTTCTTCTTAAGATGTTTATAGAGCTTTTGC 60
Qy	1490 CAGAGATGTAGGTTTAAACATTCGAATAAATGATCTGCCACCAAGGGATGGAATGT 1549
Db	61 CAGAGATGTAGGTTTAAACATTCGAATAAATGATCTGCCACCAAGGGATGGAATGT 120
Qy	1550 GGGATGTAACATTCACATATTTTGCATGAATCTGTTTTCGATATATTTTAAAAA 1609
Db	121 GGGATGTAACATTCACATATTTTGCATGAATCTGTTTTCGATATATTTTAAAAA 180
Qy	1610 CTGTTTTHAGAAAATCTGGGAAGAGGAGAAATAGTGTTCCTTCAATTTGATGCAGATATTT 1669
Db	181 CTGTTTTHAGAAAATCTGGGAAGAGGAGAAATAGTGTTCCTTCAATTTGATGCAGATATTT 240
Qy	1670 GCACATGTTTGGGCAAAAGCAGAACATATCCGATACTATTTTAACTCAAGGAAAT 1729
Db	241 GCACATGTTTGGGCAAAAGCAGAACATATCCGATACTATTTTAACTCAAGGAAAT 300
Qy	1730 CTGAGATTTATCTGAACCTCATGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCT 1789
Db	301 CTGAGATTTATCTGAACCTCATGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCT 360
Qy	1790 TTGCACAGTTTGAATAATCTACTGGGGATAAATGTACATPACTGAAGACTTGTCTGAAACC 1849
Db	361 TTGCACAGTTTGAATAATCTACTGGGGATAAATGTACATPACTGAAGACTTGTCTGAAACC 420
Qy	1850 CATCTATATTCAGAGGCAAAAGCTAAGGAGACTAGTCATATTTCTGCTGGGGTATGATA 1909
Db	421 CATCTATATTCAGAGGCAAAAGCTAAGGAGACTAGTCATATTTCTGCTGGGGTATGATA 480
Qy	1910 CCAATGATCTTGAACAGAGGAAATGAAGAACTTGGAGTTAAATGCTCTAATTTATG 1969
Db	481 CCAATGATCTTGAACAGAGGAAATGAAGAACTTGGAGTTAAATGCTCTAATTTATG 540
Qy	1970 ATAGATATATGATTTGGATGCTGAACCAACCAATATATTTCCAAAGTGAGCAATTTGGAAC 2029
Db	541 ATAGATATATGATTTGGATGCTGAACCAACCAATATATTTCCAAAGTGAGCAATTTGGAAC 600
Qy	2030 GCCTGAAGCAGAAATGCGAGCTTAAAGAGCTGTTGTGTGCCACCTGTAGCCGCTTTG 2089
Db	601 GCCTGAAGCAGAAATGCGAGCTTAAAGAGCTGTTGTGTGCCACCTGTAGCCGCTTTG 660
Qy	2090 TTCCCTCATCTTGTGTGGGAGTCTGATATCCATGCGATGCCAACGGCAATTCATAACG 2149
Db	661 TTCCCTCATCTTGTGTGGGAGTCTGATATCCATGCGATGCCAACGGCAATTCATAACG 720
Qy	2150 TGGAGATGCTTAGTTTTATGACAGAGGTTCATTTTGGGGGGTGCACCG-CTGTTCCT 2208
Db	721 TGGAGATGCTTAGTTTTATGACAGAGGTTCATTTTGGGGGGTGCACCGCTGTTCCT 780
Qy	2209 GGGTATTCATTTTTCATCACTGAGCAATTTGTTG-...ATCTATGCCCTTTTGGGCTTCTCAGT 2265
Db	781 GGGTATTCATTTTTCATCACTGAGCAATTTGTTG-...ATCTATGCCCTTTTGGGCTTCTCAGT 840
Qy	2266 TCAATGAAGCAAT--AATGAAGTATTTAACT-CTTTCACTACAG-TTCTTCAAGATGTC 2321
Db	841 TTCATGAAGCAATTAATGGAGGTATTTAACTCCTTTCTACAGTTCTTCTCAAGATGTC 900
Qy	2322 TATTTAAATTAATCTTGGCC 2339
Db	901 TAAITAAAATACTTTGGC 918

RESULT 14
CR623938
LOCUS
DEFINITION
811 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS00B002YJ01 of Neuroblastoma Cot
10-normalized of Homo sapiens (human).

ACCESSION	CR623938
VERSION	CR623938.1
KEYWORDS	HTC; CNSLT_cDNA
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 811) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue 2 (bases 1 to 811) Genoscope. Direct Submission Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES	Location/Qualifiers
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Query Match	25.2%; Score 809.4; DB 3; Length 811;
Best Local Similarity	99.9%; Pred. No. 6.6e-177;
Matches	810; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	2372 AGAAAATTTATGTTAGTAAATAAATAATTTTAAACTAAATAATATAAATCTATAATGTT 2431
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Qy	2432 AAACATATGTTTCAATTAAGCATAGCACTTGAATTAACATATATAAATAGTCATATTT 2491
Db	61 AAACATATGTTTCAATTAAGCATAGCACTTGAATTAACATATATAAATAGTCATATTT 120
Qy	2492 ACATTTACAGCTTTTCATTTTGATCAGGTCTGAAATCTTTAGCACCTTAAGGAAATGACTA 2551
Db	121 ACATTTACAGCTTTTCATTTTGATCAGGTCTGAAATCTTTAGCACCTTAAGGAAATGACTA 180
Qy	2552 TGCATAATTAACCTGACCAATGAAAAAATAAGTACCTCAAAATGCAATTTGCACTGG 2611
Db	181 TGCATAATTAACCTGACCAATGAAAAAATAAGTACCTCAAAATGCAATTTGCACTGG 240
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Qy	2672 ACATGCACACACACCACTTTTTCATTCAGTATGAACCTTGAGGCTGCTGCCATTTTCCAC 2731
Db	301 ACATGCACACACACCACTTTTTCATTCAGTATGAACCTTGAGGCTGCTGCCATTTTCCAC 360
Qy	2732 TTAACCAACACAGCCTGAAGGTGAACCTCGAAAACCTTGTTTTCATAAATCTTTCAAAAGTTG 2791
Db	361 TTAACCAACACAGCCTGAAGGTGAACCTCGAAAACCTTGTTTTCATAAATCTTTCAAAAGTTG 420
Qy	2792 TTTTACATCAATGTATAAATTTCAAAATGCTCGAGGTAATTTTAATGTATAAATATATAG 2851
Db	421 TTTTACATCAATGTATAAATTTCAAAATGCTCGAGGTAATTTTAATGTATAAATATATAG 480
Qy	2852 TAAGAAAAGTATGTTATGTCATCTTAGTATAGATCAACATACAAATTCATCAATCA 2911

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Db 481 TAAGAAAAGTATGTAATGTCATCTTAGTAGAATAGATCACAACATAAAATTCATTC 540
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Db 541 GTGCATGCTTTAGGTGTTAAAGCATGAGATTTGACATGTTTACTGTTAGGTCTTGCATCT 600
Qy 2972 GTGGTGCTAGGTGATGAGAGATGTCAGGACTGAGCGATTTTGTGCTCTAAAAA 3031
Db 601 GTGGTGCTAGGTGATGAGAGATGTCAGGACTGAGCGATTTTGTGCTCTAAAAA 660
Qy 3032 AAAAGCGCTTTGTAGGCGTTTAAATATGCTTATTTGTGCTCTCTACCTACCTATTA 3091
Db 661 AAAAGCGCTTTGTAGGCGTTTAAATATGCTTATTTGTGCTCTCTACCTACCTATTA 720
Qy 3092 CACACTGTTGCTTTGTGGGTTTGTGTTGATGCGGTGTTTATATACAGTAGTTAAATTC 3151
Db 721 CACACTGTTGCTTTGTGGGTTTGTGTTGATGCGGTGTTTATATACAGTAGTTAAATTC 780
Qy 3152 CATGCAGAAAAATAAATGCTCGTAATTC 3182
Db 781 CATGCAGAAAAATAAATGCTCGTAATTC 811

RESULT 15
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LOCUS AL520917 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DB002VJ01 5-PRIME, mRNA sequence.
ACCESSION AL520917
VERSION AL520917.3 GI:45696403
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:31039233.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9838.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DB002CE01QP1&c=9838.r.
FEATURES
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1..811
Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo (dT)
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digested with Not I and EcoR V sites of the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 24.9%; Score 799.8; DB 1; Length 811;
Best Local Similarity 98.8%; Pred. No. 1.1e-174;
Matches 801; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Db 1 AGAAAAATTTATGGTGTAGTATATAAATATTTTAACTAAATATATAAATCTATTAATGTT 60
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Db 121 ACACCTACAGCTTTTCATTTGATCAGGTCTGAAATCTTTAGCAGCTTAGGAAAATGACTA 180
Qy 2552 TGCATAATTTATACCTGACCATGAAAAAATAAGTACCTCAATGATGATGCAATTTGCACTGG 2611
Db 181 TGCATAATTTATACCTGACCATGAAAAAATAAGTACCTCAATGATGATGCAATTTGCACTGG 240
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Db 241 TGATTTCAAATGCGCAAAATCTTTGTGCCATCTTGTATATAGGTATTTTTCATCGGTTG 300
Qy 2672 ACATGCACACAAACCATTTTCATTCAGTATGAACCTTGAGGCTGCGCCATTTTCCAC 2731
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Qy 2732 TTAACCAAAACAGCTGAAAGGTGAACCTCGAAACCTGTTTTCATAAATCTTTCAAAAGTTG 2791
Db 361 TTAACCAAAACAGCTGAAAGGTGAACCTCGAAACCTGTTTTCATAAATCTTTCAAAAGTTG 420
Qy 2792 TTTTACATCAATGTTTAAATTTCAAATGCTGCAAGGTAAATTAATGTATATAAATATTAG 2851
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Db 541 GTGCATGCTTTTAGGTGTTTAAAGCATGAGATTTGACATGTTTACTGTTAGGTCTTGCATCT 600
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Db 601 GTGGTGCTAGGTGATGAGAGATGTCAGGACTGAGCGATTTTGTGCTCTAAAAA 660
Qy 3032 AAAAGCGCTTTGTAGGCGTTTAAATATGCTTATTTGTGCTCTCTACCTACCTATTA 3091
Db 661 AAAAGCGCTTTGTAGGCGTTTAAATATGCTTATTTGTGCTCTCTACCTACCTATTA 720
Qy 3092 CACACTGTTGCTTTGTGGGTTTGTGTTGATGCGGTGTTTATATACAGTAGTTAAATTC 3151
Db 721 CACACTGTTGCTTTGTGGGTTTGTGTTGATGCGGTGTTTATATACAGTAGTTAAATTC 780
Qy 3152 CATGCAGAAAAATAAATGCTCGTAATTC 3182
Db 781 CATGCAGAAAAATAAATGCTCGTAATTC 811
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Search completed: July 2, 2005, 19:42:19
Job time : 9990 secs

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Db 241 AATCCTCAAAATGCTGTGGCTCTCTTTCGAGAGAAATGACACAGGTGAAGCATGCTATGG 300
Qy 301 AAAGCAACCATTTGACTCAGTAGAGGAGTATCAGTTCAGTATCGCTACTCTTCAAGGGTAC 360
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Qy 541 ATAAGATTACGTTTGCATTAATCTGAAATACTCTGTGCAATAACCAAGMAAAATTA 600
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Qy 721 GACAAATGAGTTCAAGTGCAGGCAATTCACAGCGAGTGTGTATGGCTTCAGCCTGAT 780
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Qy 781 CGTTGGACAGAGTACAGCATACAGACGATGGAACCAAGATAACCTTGAATCTTTGAT 840
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Qy 841 TTTTTCGAAGAGATCTCAGTGAGCAGTGTTCAGGGTATGCCCTTCCTGGACATGTG 900
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Db 1321 TTTGAAATTTCCAGTAAAGAAATTAACATTTGACCACCTCCAGTTGTTAAAGCTCACTCAT 1380
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Db 1381 GTGACTGCATCGAAATCTAAGGATCGGAAAGAAATCTGTGGTTTCAGAGAGAAATTCCTTT 1440
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Db 1441 TCAGAAATCAGCCATTTCTTCTCTTAAGATGGTTTTAGAGTCTTTGCGCAGAGATGTA 1500
Qy 1501 GGGTTTAAACATTTGAATAAAATGGATCTGCCAGCAAGGGATGGAAATGTGGATGTAAAC 1560
Db 1501 GGGTTTAAACATTTGAATAAAATGGATCTGCCAGCAAGGGATGGAAATGTGGATGTAAAC 1560
Qy 1561 TTATCAACATATTTTGACATGAATCTGTTTTGGATATAAATTTAAATACTGTTTTAGAA 1620
Db 1561 TTATCAACATATTTTGACATGAATCTGTTTTGGATATAAATTTAAATACTGTTTTAGAA 1620
Qy 1621 AATCTGGGAAGAGGAGAAATAGTGTCTTCAATTTGATGCGAGATATTTGCAATGGTT 1680
Db 1621 AATCTGGGAAGAGGAGAAATAGTGTCTTCAATTTGATGCGAGATATTTGCAATGGTT 1680
Qy 1681 CGGCAAAACGAGAAACAAATATCCGATACTATTTTAACTCAAGGAAATCTCAGATTTAT 1740
Db 1681 CGGCAAAACGAGAAACAAATATCCGATACTATTTTAACTCAAGGAAATCTCAGATTTAT 1740
Qy 1741 CCTGAACTCATGGACCTCAGATCTCGGACAAACCCCATTTGCAATGAGCTTTGCACAGTTT 1800
Db 1741 CCTGAACTCATGGACCTCAGATCTCGGACAAACCCCATTTGCAATGAGCTTTGCACAGTTT 1800
Qy 1801 GAAAACTCTA CTGGGATATAATGTATCATCTGAAGACTTCTCAGAAACCATCTATAT 1860
Db 1801 GAAAACTCTA CTGGGATATAATGTATCATCTGAAGACTTCTCAGAAACCATCTATAT 1860
Qy 1861 CAAGGCGCAAAAGCTAAGGAGCTAGTCATATTTCTGCTGGGGTGAATACCAATGATCCT 1920
Db 1861 CAAGGCGCAAAAGCTAAGGAGCTAGTCATATTTCTGCTGGGGTGAATACCAATGATCCT 1920
Qy 1921 GAAAACAGAAGGAAATTTGAAGGAACTTTGGAGTTAATGGTCTAATTTATGATAGGATATAT 1980
Db 1921 GAAAACAGAAGGAAATTTGAAGGAACTTTGGAGTTAATGGTCTAATTTATGATAGGATATAT 1980
Qy 1981 GATTTGATGCTGAAACAAACCAATATATTTCAAGTGGAGCAATTTGAAACGCCTGAAAGCAG 2040
Db 1981 GATTTGATGCTGAAACCAACCAATATATTTCAAGTGGAGCAATTTGAAACGCCTGAAAGCAG 2040
Qy 2041 GAATTTGCCAGAGCTTAAGAGCTGTTGTGTCACACTGTTAGCCGCTTTGTTCCCTCATCT 2100
Db 2041 GAATTTGCCAGAGCTTAAGAGCTGTTGTGTCACACTGTTAGCCGCTTTGTTCCCTCATCT 2100
Qy 2101 TTGTGTGGGAGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTTGGAGAAATGCT 2160
Db 2101 TTGTGTGGGAGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTTGGAGAAATGCT 2160
Qy 2161 TAGTTTTTATTTGCAACAGAGGTCAATTTTGGGGGCGTGACCGCTGTTCTGGGTATTCATTT 2220
Db 2161 TAGTTTTTATTTGCAACAGAGGTCAATTTTGGGGGCGTGACCGCTGTTCTGGGTATTCATTT 2220
Qy 2221 TTCAATCATGAGCAATTTGTCATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAA 2280
Db 2221 TTCAATCATGAGCAATTTGTCATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAA 2280
Qy 2281 TGAAGTATTTAACTCTTCTTCACTAGTCTTTCGAAAGTATGCTATTTAAATTTACTTGGCCA 2340
Db 2281 TGAAGTATTTAACTCTTCTTCACTAGTCTTTCGAAAGTATGCTATTTAAATTTACTTGGCCA 2340
Qy 2341 GGTATAATTTGCCAGTCACTCTTTATAGTGAGAAATTTTATGGTTAGTAAATAAATA 2400
Db 2341 GGTATAATTTGCCAGTCACTCTTTATAGTGAGAAATTTTATGGTTAGTAAATAAATA 2400

Db 601 AAAAAATCTAGATTTAGGGTGAAGCTGACACTAGAAGGCCTGGAGGAAGATGACGATGAT 660
Qy 661 AGGGTATCTCCCATCTGCTACTCCACAAAATGTCCTAATAGCTGGAGATATCTCTTAATAAGC 720
Db 661 AGGGTATCTCCCATCTGCTACTCCACAAAATGTCCTAATAGCTGGAGATATCTCTTAATAAGC 720
Qy 721 GACAAATGAGTTCAAGTGCAGGCATTTACAGCCGGAGTGTGGTTATGCTTGGCTTGCAGCCTGAT 780
Db 721 GACAAATGAGTTCAAGTGCAGGCATTTCAAGCCGGAGTGTGGTTATGCTTGGCTTGCAGCCTGAT 780
Qy 781 CGTTGGACAGAGTACAGCATACAGACGATGGAAACAGATAACCTGGAACTAAATCTTTGAT 840
Db 781 CGTTGGACAGAGTACAGCATACAGACGATGGAAACAGATAACCTGGAACTAAATCTTTGAT 840
Qy 841 TTTTTCGAAGAAGATCTCAGTGCAGCAGTGTCTCAGGGTGATGCCCTTCTCGAGCATGTG 900
Db 841 TTTTTCGAAGAAGATCTCAGTGCAGCAGTGTCTCAGGGTGATGCCCTTCTCGAGCATGTG 900
Qy 901 GGTACAGCTTGTCTCTTATCATCCACCATTGCTGAGAGTGGAAAGTGTGGAAATCTTT 960
Db 901 GGTACAGCTTGTCTCTTATCATCCACCATTGCTGAGAGTGGAAAGTGTGGAAATCTTT 960
Qy 961 ACTCTTCCCATCATGAGCAGAAATTTCCCGGAAAACAAATAGGCAAAAGTGAGAGTTGACTAT 1020
Db 961 ACTCTTCCCATCATGAGCAGAAATTTCCCGGAAAACAAATAGGCAAAAGTGAGAGTTGACTAT 1020
Qy 1021 ATAATTAATTAAGCCATTAACAGGATACAGTTGTGACATGAATACTTCAATTTTCCAAGTAT 1080
Db 1021 ATAATTAATTAAGCCATTAACAGGATACAGTTGTGACATGAATACTTCAATTTTCCAAGTAT 1080
Qy 1081 TGGAAAGCAAGATACCAATTTGGATGTTGGCCATCGAGGTGAGGAACTCTTACAACT 1140
Db 1081 TGGAAAGCAAGATACCAATTTGGATGTTGGCCATCGAGGTGAGGAACTCTTACAACT 1140
Qy 1141 GCCAGCTGGCTTAAAGTTCAAGAAATACTATGCTTCTTAAAGAAATGCTGCTAGTCAAT 1200
Db 1141 GCCAGCTGGCTTAAAGTTCAAGAAATACTATGCTTCTTAAAGAAATGCTGCTAGTCAAT 1200
Qy 1201 GGTGAGCCTTGTAGAAATTTGACGTACACCTTTTCAAGAGGACTTTGTGCCCGTGGTATAT 1260
Db 1201 GGTGAGCCTTGTAGAAATTTGACGTACACCTTTTCAAGAGGACTTTGTGCCCGTGGTATAT 1260
Qy 1261 CATGATCTTACCTGTTGTTGCTATGAAAGAAATTTGATGCTGATCCAGTTGAAATTA 1320
Db 1261 CATGATCTTACCTGTTGTTGCTATGAAAGAAATTTGATGCTGATCCAGTTGAAATTA 1320
Qy 1321 TTTGAAATTCAGTAAAGAAATTAACATTTGACCAACTCCAGTTGCTTAAAGCTCACTCAT 1380
Db 1321 TTTGAAATTCAGTAAAGAAATTAACATTTGACCAACTCCAGTTGCTTAAAGCTCACTCAT 1380
Qy 1381 GTGACTGCACTGAAATCTTAAGGATCGGAAAGAAATCTGTGGTTTCAGGAGGAAATTTCTTTT 1440
Db 1381 GTGACTGCACTGAAATCTTAAGGATCGGAAAGAAATCTGTGGTTTCAGGAGGAAATTTCTTTT 1440
Qy 1441 TCAGAAATTCAGCCTTCTCTCTTAAGATGGTTTATAGTCTTTTGGCAGAGATGTA 1500
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Qy 1501 GGGTTTAAATTAAGTAAATGGATCTGCCAGCAAGGATGGAAATGGGATGGTAAAC 1560
Db 1501 GGGTTTAAATTAAGTAAATGGATCTGCCAGCAAGGATGGAAATGGGATGGTAAAC 1560
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Db 1561 TTATCAACATATTTTGCATGAATCTGTTTGGATATAATTTTAAAACTGTTTTAGAA 1620
Qy 1621 AATTTCTGGGAAGAGGAAATAGTGGTTTCTTCAATTTGATGCGAGATTTTGGCAATGGTT 1680
Db 1621 AATTTCTGGGAAGAGGAAATAGTGGTTTCTTCAATTTGATGCGAGATTTTGGCAATGGTT 1680
Qy 1681 CGGCAAAAGCAGAAACAAATATCCGATACTATTTTAACTCAAGGAAATCTCGAGATTTAT 1740
Db 1681 CGGCAAAAGCAGAAACAAATATCCGATACTATTTTAACTCAAGGAAATCTCGAGATTTAT 1740

Qy 1741 CCTGAATCATGGACCTCAGATCTCGGCAACCCCCATTTGCAATGAGCTTTGCAAGTTT 1800
Db 1741 CCTGAATCATGGACCTCAGATCTCGGCAACCCCCATTTGCAATGAGCTTTGCAAGTTT 1800
Qy 1801 GAAAAATCTACTGGGGATAAATGTACATCTGAAGACTTGTCTCAGAAAACCCATCTTATAT 1860
Db 1801 GAAAAATCTACTGGGGATAAATGTACATCTGAAGACTTGTCTCAGAAAACCCATCTTATAT 1860
Qy 1861 CAAGAGGCAAAAGCTTAAAGGACTAGTCAATTTCTGCTGGGGTGAATACCAATGATCCT 1920
Db 1861 CAAGAGGCAAAAGCTTAAAGGACTAGTCAATTTCTGCTGGGGTGAATACCAATGATCCT 1920
Qy 1921 GAAAAACAGAGAAATTTGAAGGAACTTGGAGTAAATGTCTAAATTTATGATAGGATATAT 1980
Db 1921 GAAAAACAGAGAAATTTGAAGGAACTTGGAGTAAATGTCTAAATTTATGATAGGATATAT 1980
Qy 1981 GATTTGGATCCCTGAAACCAAAATATATTTCAAAGTGGAGCAATTTGGAACCCCTGAAGCAG 2040
Db 1981 GATTTGGATCCCTGAAACCAAAATATATTTCAAAGTGGAGCAATTTGGAACCCCTGAAGCAG 2040
Qy 2041 GAAATGCCAGAGCTTAAAGGCTGTTGTGTCACCTGTTAGCCGCTTTGTTCCCTCATCT 2100
Db 2041 GAAATGCCAGAGCTTAAAGGCTGTTGTGTCACCTGTTAGCCGCTTTGTTCCCTCATCT 2100
Qy 2101 TTTGTGGGGAGTCTGATATCCATGTGGATGCAACGGCAATTTGATAACGTTGAGAAATGCT 2160
Db 2101 TTTGTGGGGAGTCTGATATCCATGTGGATGCAACGGCAATTTGATAACGTTGAGAAATGCT 2160
Qy 2161 TAGTTTTTATTTGCACAGAGGTCAATTTTGGGGGGTGCACCGCTGTTCTGGGTATTCAATTT 2220
Db 2161 TAGTTTTTATTTGCACAGAGGTCAATTTTGGGGGGTGCACCGCTGTTCTGGGTATTCAATTT 2220
Qy 2221 TTCAATCACTGAGCAATTTGATCTATGCTTCTGAGTTCCTCAATGAAGCAATAA 2280
Db 2221 TTCAATCACTGAGCAATTTGATCTATGCTTCTGAGTTCCTCAATGAAGCAATAA 2280
Qy 2281 TGAAGTATTTAACTCTTTTCACTACAGTCTCTGCAAGTATGCTATTTAAATTTACTTTGGCCA 2340
Db 2281 TGAAGTATTTAACTCTTTTCACTACAGTCTCTGCAAGTATGCTATTTAAATTTACTTTGGCCA 2340
Qy 2341 GGTATAAATTTGCCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTATATAAATA 2400
Db 2341 GGTATAAATTTGCCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTATATAAATA 2400
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Qy 2461 TTGAAATTTAACTATATAAATAGCTCATATTTACACTTTACAGCTTTTCAATTTGATCAGGTC 2520
Db 2461 TTGAAATTTAACTATATAAATAGCTCATATTTACACTTTACAGCTTTTCAATTTGATCAGGTC 2520
Qy 2521 TGAAATCTTTTAGCATTAAAGGAAAATGACTATGCAATAATTTATACCTGACCATGAAAATA 2580
Db 2521 TGAAATCTTTTAGCATTAAAGGAAAATGACTATGCAATAATTTATACCTGACCATGAAAATA 2580
Qy 2581 TAAGTACCTCAAAATGATGATTTGCACTGCTGATTTCCAACTGCAAAAATCTTTTGCCCA 2640
Db 2581 TAAGTACCTCAAAATGATGATTTGCACTGCTGATTTCCAACTGCAAAAATCTTTTGCCCA 2640
Qy 2641 TCTTGTATATAGGTATTTTTTACATGGTTTGAATGCAACACCACTTTTCAATTTTCAATCAGT 2700
Db 2641 TCTTGTATATAGGTATTTTTTACATGGTTTGAATGCAACACCACTTTTCAATTTTCAATCAGT 2700
Qy 2701 ATGAACCTTGGAGTCTGCTGCAATTTTCCACTTTAAACCAAAACCCAGCTGGAAGTGAACCTC 2760
Db 2701 ATGAACCTTGGAGTCTGCTGCAATTTTCCACTTTAAACCAAAACCCAGCTGGAAGTGAACCTC 2760
Qy 2761 GAAACTTGTCTTCAAAAATCTTTTCAAAAGTGTGTTTTTACATCAATGTTTAAATTTTCAAAATG 2820
Db 2761 GAAACTTGTCTTCAAAAATCTTTTCAAAAGTGTGTTTTTACATCAATGTTTAAATTTTCAAAATG 2820

319	Db		ATGCTGTGGCTCTTCTTCCAGAGATGACACAGGTGAAAGCATGCTATGGAAAGCAACCA	378
311	Qy		TTGTACTCAGTAGAGAGATCAGTTTCTAGTATCGTACTTCAAAGGTACTTTTTAGAAC	370
379	Db		TTGTACTCAGTAGAGAGATCAGTTTCTAGTATCGTACTTCAAAGGTACTTTTTAGAAC	438
371	Qy		CAAAGACTATCGTGGTCCATCTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC	430
439	Db		CAAAGACTATCGTGGTCCATCTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAC	498
431	Qy		CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTATTGACGATGGACAATTTGGAAATCC	490
499	Db		CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTATTGACGATGGACAATTTGGAAATCC	558
491	Qy		ACAATGGTGTGAAACTCTCGGATCTTGATGGCTGACATGTCAGACTGAAATAAGATTAC	550
559	Db		ACAATGGTGTGAAACTCTCGGATCTTGATGGCTGACATGTCAGACTGAAATAAGATTAC	618
551	Qy		GTTTGCATTTCTGAAAAACCTTCGTGCTCAATAACCAAGAAAAAATTTAAAAAAATCTTA	610
619	Db		GTTTGCATTTCTGAAAAACCTTCGTGCTCAATAACCAAGAAAAAATTTAAAAAAATCTTA	678
611	Qy		GATTTAGGGTGAAGCTGACACTAGAAAGGCTTGGAGGAAGATGACGATGATAGGGTATCTC	670
679	Db		GATTTAGGGTGAAGCTGACACTAGAAAGGCTTGGAGGAAGATGACGATGATAGGGTATCTC	738
671	Qy		CCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTTAATACGCGACAATGAGT	730
739	Db		CCACTGTACTCCACAAAATGTCCAATAGCTTGGAGATATCCTTTAATACGCGACAATGAGT	798
731	Qy		TCAAAGTGCAGGCATTCACAGCCGAGTGTGTTATGCTTTCAGAGCTGATCGTTGGACAG	790
799	Db		TCAAAGTGCAGGCATTCACAGCCGAGTGTGTTATGCTTTCAGAGCTGATCGTTGGACAG	858
791	Qy		AGTACAGCATACAGACGATGGAAACCGATAAACCCTGGAACTAATCTTTTGATTTTTCGAAG	850
859	Db		AGTACAGCATACAGACGATGGAAACCGATAAACCCTGGAACTAATCTTTTGATTTTTCGAAG	918
851	Qy		AAGATCTAGTAGACGATGATTTTTCAGGATGATCCCTTCTTGACAGATTTGGGTACAGCTT	910
919	Db		AAGATCTAGTAGACGATGATTTTTCAGGATGATCCCTTCTTGACAGATTTGGGTACAGCTT	978
911	Qy		GTCTCTTATCATCCACCATTCTCGAGAGTGGAAAGAGTGTGGAAATCTTACTCTTTCCCA	970
979	Db		GTCTCTTATCATCCACCATTCTCGAGAGTGGAAAGAGTGTGGAAATCTTACTCTTTCCCA	1038
971	Qy		TCATGACGAGAAATTTCCCGGAAAACAATAGCGAAAAGTGAGAGTTGACTATAATTTATTA	1030
1039	Db		TCATGACGAGAAATTTCCCGGAAAACAATAGCGAAAAGTGAGAGTTGACTATAATTTATTA	1098
1031	Qy		AGCCATTACAGAGATACAGTTTGTGACATGAAATCTTTCATTTTCCAGTATTTGAAGCCAA	1090
1099	Db		AGCCATTACAGAGATACAGTTTGTGACATGAAATCTTTCATTTTCCAGTATTTGAAGCCAA	1158
1091	Qy		GAATACCATTTGGATTTGGCCATCGAGGTGCGAGAAAACCTCAACAACCTGCCAGCTGG	1150
1159	Db		GAATACCATTTGGATTTGGCCATCGAGGTGCGAGAAAACCTCAACAACCTGCCAGCTGG	1218
1151	Qy		CTAAAGTTTCAAGAAAATCTATTGCTTTCTTTTAAGAAATGCTGCTAGTTCAGTGGTGCAGCCT	1210
1219	Db		CTAAAGTTTCAAGAAAATCTATTGCTTTCTTTTAAGAAATGCTGCTAGTTCAGTGGTGCAGCCT	1278
1211	Qy		TTGTAGAAATTTGACGTACACTTTTCAAAGGACTTTGTGCCGTGGTATATCATGATCTTA	1270
1279	Db		TTGTAGAAATTTGACGTACACTTTTCAAAGGACTTTGTGCCGTGGTATATCATGATCTTA	1338
1271	Qy		CCTGTGTTTGCATATGAAAAGAAATTTGATGCTGATCCAGTTGAAATTTATTTGAAATTC	1330
1339	Db		CCTGTGTTTGCATATGAAAAGAAATTTGATGCTGATCCAGTTGAAATTTATTTGAAATTC	1398
1331	Qy		CAGTAAAGAAATTAACATTTTCAACCAACTCCAGTTTGTAAAGCTCACTCATGTGATCCAC	1390

1399	CAGTAAAGAAATTAACAATTTTGACCAACTCCAGTTGTTTAAAGCTCACTCATGTGCTGCAC	1450
1391	TGAAATCTAAGGATCGAAAGAAATCTGTGGTTTCAGGAGGAAAAATTCCTTTTCAGAAAAATC	1450
1459	TGAAATCTAAGGATCGAAAGAAATCTGTGGTTTCAGGAGGAAAAATTCCTTTTCAGAAAAATC	1518
1451	AGCCATTTCCCTTCCTTAAGATGGTTTTAGAGTCTTTTGCCAGAGAGTGTAGGGTTTAAACA	1510
1519	AGCCATTTCCCTTCCTTAAGATGGTTTTAGAGTCTTTTGCCAGAGAGTGTAGGGTTTAAACA	1578
1511	TTGAAATAAATGGATCTGCCACGAAGGATGGAATGTGGATGGTAACTTATCAACAT	1570
1579	TTGAAATAAATGGATCTGCCACGAAGGATGGAATGTGGATGGTAACTTATCAACAT	1638
1571	ATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAACTGTTTTAGAAAAATTCCTGGGA	1630
1639	ATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAACTGTTTTAGAAAAATTCCTGGGA	1698
1631	AGAGGAAATAGTGTTCCTTCATTTTGATGCAGATATTGACAAATGTTTCGCAAAAGC	1690
1699	AGAGGAAATAGTGTTCCTTCATTTTGATGCAGATATTGACAAATGTTTCGCAAAAGC	1758
1691	AGAACAAATATCCGATACATAATTTTAACTCAAGAAATCTCAGATTTATCCTGAACTCA	1750
1759	AGAACAAATATCCGATACATAATTTTAACTCAAGAAATCTCAGATTTATCCTGAACTCA	1818
1751	TGCACTTCAGATCTCGGACAAACCCCATTTGCAATGAGCTTTGSCACAGTTTGAAAAATCTAC	1810
1819	TGCACTTCAGATCTCGGACAAACCCCATTTGCAATGAGCTTTGSCACAGTTTGAAAAATCTAC	1878
1811	TGGGGATAAATGTACATACCTGAAGACTTGTCTGAAACCCTCTATATTCAAGAGCAA	1870
1879	TGGGGATAAATGTACATACCTGAAGACTTGTCTGAAACCCTCTATATTCAAGAGCAA	1938
1871	AAGCTAAGGACTAGTGCATATCTGCTGGGGTCAATACCAATGATCCTCAAAAACAGAA	1930
1939	AAGCTAAGGACTAGTGCATATCTGCTGGGGTCAATACCAATGATCCTCAAAAACAGAA	1998
1931	GGAAATTTGAAGGAACTTGGAGTAAATGGTCTAAATTTTATGATAGGATATGATTTGATGC	1990
1999	GGAAATTTGAAGGAACTTGGAGTAAATGGTCTAAATTTTATGATAGGATATGATTTGATGC	2058
1991	CTGAAACAAACAAATATATTCAAAGTGGAGCAATTTGAAACCCCTGAGCAGGAATTCGCAG	2050
2059	CTGAAACAAACAAATATATTCAAAGTGGAGCAATTTGAAACCCCTGAGCAGGAATTCGCAG	2118
2051	AGCTTAAGAGCTTTGTGTGCCACTGTGTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2110
2119	AGCTTAAGAGCTTTGTGTGCCACTGTGTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2178
2111	AGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTGGAGAAATGCTTAGTTTTTAT	2170
2179	AGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTGGAGAAATGCTTAGTTTTTAT	2238
2171	TGCACAGAGTCAATTTTGGGGCGTGCACCGCTGTTCTGGGTTATTCATTTTTTCATCACTG	2230
2239	TGCACAGAGTCAATTTTGGGGCGTGCACCGCTGTTCTGGGTTATTCATTTTTTCATCACTG	2298
2231	AGCATTTGTGATCTATGCCCCCTTTTGGCTTCTCAGTTCAAATGAAGCAATTAATCAAGTATTT	2290
2299	AGCATTTGTGATCTATGCCCCCTTTTGGCTTCTCAGTTCAAATGAAGCAATTAATCAAGTATTT	2358
2291	AACCTTTTCACTACAGTCTTTCGCAAGTATGCTATTTAAATTACTTGGCCAGGTATAATTG	2350
2359	AACCTTTTCACTACAGTCTTTCGCAAGTATGCTATTTAAATTACTTGGCCAGGTATAATTG	2418
2351	CCAGTCAGTCTCTTTATAGTGAGAAAAATTTATGTTAGTAAATATTAATTTTTAAACTA	2410
2419	CCAGTCAGTCTCTTTATAGTGAGAAAAATTTATGTTAGTAAATATTAATTTTTAAACTA	2478
2411	AATATATAAATCTATAATGTTTAAACATATGTTTCATTTAAAGCATAGCACTTTGAAATTA	2470
2479	AATATATAAATCTATAATGTTTAAACATATGTTTCATTTAAAGCATAGCACTTTGAAATTA	2538

QY 971 TCATGACGAGAAATCCGGGAAACAATAGCAGGAGTGAGATTGACTATATATATTA 1030
Db 1047 TCATGACGAGAAATCCGGGAAACAATAGCAGGAGTGAGATTGACTATATATTA 1106
QY 1031 AGCCATTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCAAGTATGGAAGCCAA 1090
Db 1107 AGCCATTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCAAGTATGGAAGCCAA 1166
QY 1091 GAATACCATTTGGATGTTGGCCATCGAGGTGCAGGAACTCTACAAACAATGCCAGCTGG 1150
Db 1167 GAATACCATTTGGATGTTGGCCATCGAGGTGCAGGAACTCTACAAACAATGCCAGCTGG 1226
QY 1151 CTAAGTTCAAGAAATACATTTGCTTCTTTAAGAAATGCTGCTAGTCATGTTGACGCT 1210
Db 1227 CTAAGTTCAAGAAATACATTTGCTTCTTTAAGAAATGCTGCTAGTCATGTTGACGCT 1286
QY 1211 TTGTAGAAATTTGACGTACACCTTTCAAGGACTTTTGGCCGTGATATCATGATCTTA 1270
Db 1287 TTGTAGAAATTTGACGTACACCTTTCAAGGACTTTTGGCCGTGATATCATGATCTTA 1346
QY 1271 CCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTAATTTGAAATTC 1330
Db 1347 CCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTAATTTGAAATTC 1406
QY 1331 CAGTAAAGAAATTAACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCAC 1390
Db 1407 CAGTAAAGAAATTAACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCAC 1466
QY 1391 TGAATCTTAAGATCGGAAGAACTGTGGTTTCAGGAGGAAATTCCTTTTCAGAAATC 1450
Db 1467 TGAATCTTAAGATCGGAAGAACTGTGGTTTCAGGAGGAAATTCCTTTTCAGAAATC 1526
QY 1451 AGCCATTTCTTCTTAAGATGTTTGTAGAGTCTTTTGCAGAGAGATGTAGGGTTTAAACA 1510
Db 1527 AGCCATTTCTTCTTAAGATGTTTGTAGAGTCTTTTGCAGAGAGATGTAGGGTTTAAACA 1586
QY 1511 TTGAAATAAATGGATCTGCCAGCAAGGATGGAATGTGGATGGTAACTTATCAACAT 1570
Db 1587 TTGAAATAAATGGATCTGCCAGCAAGGATGGAATGTGGATGGTAACTTATCAACAT 1646
QY 1571 ATTTTGACATGATCTGTTTCTTCAATTTGATGAGATATTTTGAACCTGTTTGAAGAAATCTCGGA 1630
Db 1647 ATTTTGACATGATCTGTTTCTTCAATTTGATGAGATATTTTGAACCTGTTTGAAGAAATCTCGGA 1706
QY 1631 AGAGGAGAAATAGTGTCTTCTTCAATTTGATGAGATATTTTGAACCTGTTTGAAGAAATCTCGGA 1690
Db 1707 AGAGGAGAAATAGTGTCTTCTTCAATTTGATGAGATATTTTGAACCTGTTTGAAGAAATCTCGGA 1766
QY 1691 AGAACCAATATCCGATACCTATTTTAACTCAAGGAAATCTGAGATTTATCCTGAATCTCA 1750
Db 1767 AGAACCAATATCCGATACCTATTTTAACTCAAGGAAATCTGAGATTTATCCTGAATCTCA 1826
QY 1751 TGGACCTCAGATCTCGGACCAACCCCATTTGCAATGAGCTTTGACAGTTTGAAGAAATCTTAC 1810
Db 1827 TGGACCTCAGATCTCGGACCAACCCCATTTGCAATGAGCTTTGACAGTTTGAAGAAATCTTAC 1886
QY 1811 TGGGATAAATGACATCTGAAGACTTGTCTCAGAAACCCATCTTATATTCAGAGGCCAA 1870
Db 1887 TGGGATAAATGACATCTGAAGACTTGTCTCAGAAACCCATCTTATATTCAGAGGCCAA 1946
QY 1871 AAGCTAAGGGAAGTGTATCTGCTGGGTGATGATCAACCAATGATCCTGAAACAGAA 1930
Db 1947 AAGCTAAGGGAAGTGTATCTGCTGGGTGATGATCAACCAATGATCCTGAAACAGAA 2006
QY 1931 GGAATTTGAAGAACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATTTGGATGC 1990
Db 2007 GGAATTTGAAGAACTTGGAGTTAATGGTCTAATTTATGATAGGATATATGATTTGGATGC 2066
QY 1991 CTGAACCAACCAATATATTTCCAGTGGAGCAATTCGAAGCCCTGAAGAGGAATTTGCCAG 2050
Db 2067 CTGAACCAACCAATATATTTCCAGTGGAGCAATTTGAAGCCCTGAAGAGGAATTTGCCAG 2126
QY 2051 AGCTTAAAGAGCTGTTGTGTGCCACTGTTAGCCGCTTTGTTCCTCATCTTTGTGTGGGG 2110

Db 2127 AGCTTAAAGAGCTGTTGTGTGCCACTGTTAGCCGCTTTGTTCCTCATCTTTGTGTGGGG 2186
QY 2111 AGTCTGATATCCATGTGGATGCCAAGCAATGATAAAGTGAGAAATGCTTGTATTTTAT 2170
Db 2187 AGTCTGATATCCATGTGGATGCCAAGCAATGATAAAGTGAGAAATGCTTGTATTTTAT 2246
QY 2171 TGCACAGAGGTCATTTTGGGGCGTGCAACCGCTGTTCTGGGTATTCATTTTTCACACTG 2230
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QY 2231 AGCATTTGTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAAATGAAGTATTT 2290
Db 2307 AGCATTTGTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAAATGAAGTATTT 2366
QY 2291 AACTCTTTCACTACAGTCTTGTGCAAGTATGCTATTTAAATTAATTTGCGCCAGGTATAATTG 2350
Db 2367 AACTCTTTCACTACAGTCTTGTGCAAGTATGCTATTTAAATTAATTTGCGCCAGGTATAATTG 2426
QY 2351 CCAAGTCAGTCTCTTTATAGTGAGAAATTTATTTGGTTAGTAAATATAAATTTTAAACTA 2410
Db 2427 CCAAGTCAGTCTCTTTATAGTGAGAAATTTATTTGGTTAGTAAATATAAATTTTAAACTA 2486
QY 2411 AATATATAAATCTATTAATCTTAAACATATGTTTCAATTAAGCATAGCACTTTGAAATTA 2470
Db 2487 AATATATAAATCTATTAATCTTAAACATATGTTTCAATTAAGCATAGCACTTTGAAATTA 2546
QY 2471 CTATATAAATAGCTCATATTTTACATTTACATTTACAGCTTTTCAATTTGATCAGGTCGAAATCTTT 2530
Db 2547 CTATATAAATAGCTCATATTTTACATTTACATTTTCAATTTGATCAGGTCGAAATCTTT 2606
QY 2531 AGCACTTAAGGAAATGACTATGCAATATATACCTGACCATTGAAATTAAGTACCTC 2590
Db 2607 AGCACTTAAGGAAATGACTATGCAATATATACCTGACCATTGAAATTAAGTACCTC 2666
QY 2591 AAATGATGATGATTTGACATGTTGATTTCCAACTGCACAAATCTTTTGTGCCATCTTGTATAT 2650
Db 2667 AAATGATGATGATTTGACATGTTGATTTCCAACTGCACAAATCTTTTGTGCCATCTTGTATAT 2726
QY 2651 AGGTATTTTATACATGGGTTGACATGACACACACCATTTTCAATTCAGTATGAACCTTG 2710
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QY 2711 AGGCTGCTGCCATTTTTCACATTAACCAACCGCTGAGGTGAACCTCGAAATCTGTT 2770
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QY 2771 TCATAAATCTTTCAAAAGTTGTTTATCATCAATGTTTAAATTTCAAAATGCTCGAGGTA 2830
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QY 2831 ATTTAATGTATAAATAATTTAGTAAAGAAAGTATGTTTGCATATCTTAGTGAATATGATC 2890
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QY 2891 ACAACATACAAATTCAAATTCAGTGCATGCTTTTAAAGTATGAGATGAGATTTGATGATGTT 2950
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QY 3071 TGTGCTCTCTACATCCTTATACACATGTTGCTTTTGTGGGTTTGTGTTGATGCTGCTGT 3130
Db 3147 TGTGCTCTCTACATCCTTATACACATGTTGCTTTTGTGGGTTTGTGTTGATGCTGCTGT 3206
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Qy	131	ATAAATCCATCAGAAATGACACCTTCTCAGGTGGCTTTGAAATAAGAGGAACTCTTTTAC	191
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Qy	191	CAGAGAAGTTTTTGGCATATGTGGAGCTGTGATGCTTTTGGGAACCTGGAACTCCTCAA	250
Db	251	CAGAGAAGTTTTTGGCATATGTGGAGCTGTGATGCTTTTGGGAACCTGGAACTCCTCAA	310
Qy	251	ATGCTGTGGCTCTTCTTCCAGAGAAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCA	310
Db	311	ATGCTGTGGCTCTTCTTCCAGAGAAATGACACAGGTGAAAGCATGCTATGGAAAGCAACCA	370
Qy	311	TTGTACTCAGTACAGGAGTATCAGTTTCAAGTATCGCTACTTCAAAGGGTACTTTTTAGAAC	370
Db	371	TTGTACTCAGTACAGGAGTATCAGTTTCAAGTATCGCTACTTCAAAGGGTACTTTTTAGAAC	430
Qy	371	CAAAAGCTATCGGTGGTCCATGTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAAC	430
Db	431	CAAAAGCTATCGGTGGTCCATGTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAAAC	490
Qy	431	CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTTATGACGATGGACAATTTGGAATCC	490
Db	491	CACGATCAATAACCCCTTTAGAAAGCGAAATTTATTTATGACGATGGACAATTTGGAATCC	550
Qy	491	ACAATGGTGTGAAACTCTGGATCTTGGATGGCTGACATGTCAAGTGGGAGACTCATCTACAAAC	550
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Qy	551	GTTTGCATATTTCTGAAAAACCTCTGTGTCAATAACCAAGAAAAAATTAATAAATCTTA	610
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Qy	671	CCACTGTACTCCACAAAATGTCCAATAGCTTTGGAGATATCCTTAATAAGCGACAATGAGT	730
Db	731	CCACTGTACTCCACAAAATGTCCAATAGCTTTGGAGATATCCTTAATAAGCGACAATGAGT	790
Qy	731	TCAAGTCGAGGCATTTACAGCCGAGTGTGTTATGGCTTGGAGCTGATCGTTGGACAG	790
Db	791	TCAAGTCGAGGCATTTACAGCCGAGTGTGTTATGGCTTGGAGCTGATCGTTGGACAG	850
Qy	791	AGTACAGCATACAGACGATGAAACAGATAACCTTGGAACTAATCTTTCATTTTTTCGAG	850
Db	851	AGTACAGCATACAGACGATGAAACAGATAACCTTGGAACTAATCTTTCATTTTTTCGAG	910
Qy	851	AAGATCTCAGTGAGCAGTAGTTTCAGGCTGATGCCCCTTCTCGGACATGTGGGTACAGCTT	910
Db	911	AAGATCTCAGTGAGCAGTAGTTTCAGGCTGATGCCCCTTCTCGGACATGTGGGTACAGCTT	970
Qy	911	GTCTCTTATCATCCCATTTGCTGAGAGTGAAGAGTGTGGAAATCTTACTCTTCCCA	970
Db	971	GTCTCTTATCATCCCATTTGCTGAGAGTGAAGAGTGTGGAAATCTTACTCTTCCCA	1030
Qy	971	TCATGACAGAAATTTCCCGGAAAACATAGGCAAGTGAGAGTTGACTATATAATTTATTA	1030
Db	1031	TCATGACAGAAATTTCCCGGAAAACATAGGCAAGTGAGAGTTGACTATATAATTTATTA	1090
Qy	1031	AGCCATTTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCCAAAGTATTTGGAAGCCAA	1090
Db	1091	AGCCATTTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCCAAAGTATTTGGAAGCCAA	1150
Qy	1091	GAATACCATTTGGATTTGGCCATCGAGGTGCAGGAACTCTACAACAACCTGCCAGCTGG	1150
Db	1151	GAATACCATTTGGATTTGGCCATCGAGGTGCAGGAACTCTACAACAACCTGCCAGCTGG	1210
Qy	1151	CTAAAGTTCAGAAAAATCTATTGCTCTTTTAAAGAAATGCTGCTAGTCATGGTGAGCT	1210
Db	1211	CTAAAGTTCAGAAAAATCTATTGCTCTTTTAAAGAAATGCTGCTAGTCATGGTGAGCT	1270
Qy	1211	TTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTTGTGCCGTGGTATATCATGATCTTA	1270

Db	1271	 TTGTAGAAATTTGACGTACACCTTTTCAAAGACCTTTGTGCGCGTGGTATATCATGATCTTA	1330
Qy	1271	CCGTGTTCTTTGACTATGAAAAAGAAATTTTGATGCTGATCCAGTTCGAAATATTTTGAATTC	1330
Db	1331	CCGTGTTCTTTGACTATGAAAAAGAAATTTTGATGCTGATCCAGTTCGAAATATTTTGAATTC	1390
Qy	1331	CAGTAAAGAAATTAACAATTTGACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACTGCAC	1390
Db	1391	CAGTAAAGAAATTAACAATTTGACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACTGCAC	1450
Qy	1391	TGAATCTAAGGATCGGAAGAAATCTGTGTTTCAGGAGGAAATTCCTTTTCAGAAAAATC	1450
Db	1451	TGAATCTAAGGATCGGAAGAAATCTGTGTTTCAGGAGGAAATTCCTTTTCAGAAAAATC	1510
Qy	1451	AGCCATTTCTCTCTCTTTAAGATGGTTTAAAGTCTTTTGCCAGAAGATGTAGGGTTTAAACA	1510
Db	1511	AGCCATTTCTCTCTCTTTAAGATGGTTTAAAGTCTTTTGCCAGAAGATGTAGGGTTTAAACA	1570
Qy	1511	TTGAAATTAATAATTGATCTGCCAGCAAGGATCGGAATGTGGATGTGTAATCTTCAACAT	1570
Db	1571	TTGAAATTAATAATTGATCTGCCAGCAAGGATCGGAATGTGGATGTGTAATCTTCAACAT	1630
Qy	1571	ATTTTGCATCAATCTGTTTGTGGATATAATTTTAAAAACTGTTTGAAGAAATTCCTGGGA	1630
Db	1631	ATTTTGCATCAATCTGTTTGTGGATATAATTTTAAAAACTGTTTGAAGAAATTCCTGGGA	1690
Qy	1631	AGAGGAGAATAGTGTCTTTCTTCATTTTCATCCAGATATTTGCACAATGGTTCGGCAAAAGC	1690
Db	1691	AGAGGAGAATAGTGTCTTTCTTCATTTTCATCCAGATATTTGCACAATGGTTCGGCAAAAGC	1750
Qy	1691	AGAACAAATATCCGATACTATTTTAACTCAAGGAAATCTGAGATTTAATCTCGAACTCA	1750
Db	1751	AGAACAAATATCCGATACTATTTTAACTCAAGGAAATCTGAGATTTAATCTCGAACTCA	1810
Qy	1751	TGGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCTTTTGACACAGTTTGAATAATCTAC	1810
Db	1811	TGGACCTCAGATCTCGGACAAACCCCAATTCGAATGAGCTTTTGACACAGTTTGAATAATCTAC	1870
Qy	1811	TGGGGATAAATGTATACATCTGAAGACTTGTCTCAGAAACCCATCCTATATCAAGAGGCAA	1870
Db	1871	TGGGGATAAATGTATACATCTGAAGACTTGTCTCAGAAACCCATCCTATATCAAGAGGCAA	1930
Qy	1871	AGCTTAAGGACTAGTCTATATCTCTCGGGGTGATGATACCAATGATCCTCGAAAAAGAA	1930
Db	1931	AAGCTTAAGGACTAGTCTATATCTCTCGGGGTGATGATACCAATGATCCTCGAAAAAGAA	1990
Qy	1931	CGAAATTTGAAGAACTTCGGAGTTAATGGTCTAAATTTATGATAGGATATATGATGGATGC	1990
Db	1991	CGAAATTTGAAGAACTTCGGAGTTAATGGTCTAAATTTATGATAGGATATATGATGGATGC	2050
Qy	1991	CTGAAACAAACCAATATATTTCCAGTGGAGCAATTTGGAAACGCTCAAGCAGGAATTCGCAG	2050
Db	2051	CTGAAACAAACCAATATATTTCCAGTGGAGCAATTTGGAAACGCTCAAGCAGGAATTCGCAG	2110
Qy	2051	AGCTTAAGAGCTGTTGTGTCCTCCACTGTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2110
Db	2111	AGCTTAAGAGCTGTTGTGTCCTCCACTGTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2170
Qy	2111	AGTCTGATATCCATGTGGATGCAACCGCATTTGATTAACGCTGGAGAAATGCTTAGTTTTTAT	2170
Db	2171	AGTCTGATATCCATGTGGATGCAACCGCATTTGATTAACGCTGGAGAAATGCTTAGTTTTTAT	2230
Qy	2171	TGCACAGAGGTCAATTTTGGGGGGGTGCACCGCTGTTCTGGGTATTCATTTTTTCATCACTG	2230
Db	2231	TGCACAGAGGTCAATTTTGGGGGGGTGCACCGCTGTTCTGGGTATTCATTTTTTCATCACTG	2290
Qy	2231	AGCAATTTGATCTAATGCTTTTGGGCTTCTCAGTTTCAATGAAGCAATAATGAAGTATTT	2290
Db	2291	AGCAATTTGATCTAATGCTTTTGGGCTTCTCAGTTTCAATGAAGCAATAATGAAGTATTT	2350
Qy	2291	AACTCTTTTCACTACAGTTCTTGCAGATGTCTATTTAAATTTACTTTGGCCAGGTATTAATTG	2350

Db	2351	AACTCTTCTACTACAGTTCCTTGCAGATGATGCTATTAAATTTACTTGGCCAGGTATPAATTG	2411
QY	2351	CCAGTCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTAAATATAAAATATTTTAAACTA	2410
Db	2411	CCAGTCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTAAATATAAAATATTTTAAACTA	2470
QY	2411	AAATATAAAATCTATAATGTTTAAACATATGTTTCATTTAAAGCATACGACTTTTGAAATTA	2470
Db	2471	AAATATAAAATCTATAATGTTTAAACATATGTTTCATTTAAAGCATACGACTTTTGAAATTA	2530
QY	2471	CTATATAAATAGCTCATATTTTACACTTTTACAGCTTTTTCATTTGATCAGGCTCGAAATCTTT	2530
Db	2531	CTATATAAATAGCTCATATTTTACACTTTTACAGCTTTTTCATTTGATCAGGCTCGAAATCTTT	2590
QY	2531	AGCACTTAAAGGAAAATCACTATGATCAATTAATATACCTGACATGAAAATAATAGTACCTC	2590
Db	2591	AGCACTTAAAGGAAAATGACTATGATCATTAATATACCTGACCATGAAAATAATAGTACCTC	2650
QY	2591	AAATGCGATGCAATTTGCACTGGTGATTCCTCAACTGACAAAATCTTTGTGCCATCTTGATAT	2650
Db	2651	AAATGCGATGCAATTTGCACTGGTGATTCCTCAACTGACAAAATCTTTGTGCCATCTTGATAT	2710
QY	2651	AGGTATTTTTTACATGGGTTGCACATGACACAACCACTTTTCATTCAGTATGAACTTG	2710
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QY	2771	TCATAAAATCTTTTCAAAAGTGTGTTTTACATCAATGTTTAAATTTTCAAAATGCTGCAGGTA	2830
Db	2831	TCATAAAATCTTTTCAAAAGTGTGTTTTACATCAATGTTTAAATTTTCAAAATGCTGCAGGTA	2890
QY	2831	ATTTAATGTAATAAATATTAGTAGAAAAAGTATGTTTGCATCTTACATCTTTAGTAGAATAGATC	2890
Db	2891	ATTTAATGTAATAAATATTAGTAGAAAAAGTATGTTTGCATCTTACATCTTTAGTAGAATAGATC	2950
QY	2891	ACAAATCAAAATTCATTTCAAGTCATGCTTTTAGTGTTTAAAGCATGAGATTTGTACATGTT	2950
Db	2951	ACAAATCAAAATTCATTTCAAGTCATGCTTTTAGTGTTTAAAGCATGAGATTTGTACATGTT	3010
QY	2951	TACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATCTCAAGCACTGGA	3010
Db	3011	TACTGTTAGGTCCTTGCATCTGTGGTGCTAGGTGAGTATGAGAAGATCTCAAGCACTGGA	3070
QY	3011	CGTATTTTGTGGCTTAAAAAAAAGGCTGTTTGTAGCGCTTTTAAATATGCTTATTTTG	3070
Db	3071	CGTATTTTGTGGCTTAAAAAAAAGGCTGTTTGTAGCGCTTTTAAATATGCTTATTTTG	3130
QY	3071	TGTGTCCTCACTACTATTACACACTGTTGCTTTGTGGGTTTGTTTTGTATGTCGTGT	3130
Db	3131	TGTGTCCTCACTACTATTACACACTGTTGCTTTGTGGGTTTGTTTTGTATGTCGTGT	3190
QY	3131	GTTTATACAGTAGTAAATTTTCCATCGCAAAAATAAATGCTCTGAAATCTCAAA	3184
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CQ491863	AUTHORS
LOCUS	TITLE
DEFINITION	
ACCESSION	
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KEYWORDS	
SOURCE	
ORGANISM	

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Qy	2171	TGCACAGAGTCATTTTGGGGCGCTGCACCGCTGCTTCTGGGTATTCATTTTTCATCACTG	2230
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Qy	2231	AGCATTTGTATCTATGCTTTTGGGCTTCTCAGTTCATGAAGCAATAATGAAGTATTT	2290
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Qy	2531	AGCACTTAAGGAAATGATGATGATTAATTAACCTGACCATGAAAGCAATTAAGTACCTC	2590
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Qy	2711	AGGCTGCTGCCATTTTCCACTTAACCAACAGGCTGAAAGTGAACCTCGAAGCTGTT	2770
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Qy	3011	CGTATTTTGTGCTTAAATAAAGGCTGTTTGTAGGCGTTTAAATATGCTTATTTTG	3070
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VERSION	Q0497765.1	GI:41463401	
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SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
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REFERENCE	1		
AUTHORS	Schlegel, R., Endege, W.O. and Monahan, J.E.		
TITLE	Genes differentially expressed in human prostate cancer and their use		
JOURNAL	Patent: WO 0160860-A 29632 23-AUG-2001; Millennium Predictive Medicine, Inc. (US)		
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Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3168; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
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Db	147	GGCGGGGGCGGCGGACGCGGACCTGCGGACCTAGCGAACCCGCGACGACATCAATAA	206
Qy	131	ATAAATCCATCAGATGACACCTTCTCAGTTGCTTTGAAATAAGAGGAACCTTTTAC	190
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Qy	191	CAGGAGAAAGTTTTCGGATATGTGGAAGCTGTGATGCTTTGGGAAACTCGAATCTCTCAA	250
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Qy	251	ATGCTGTGGCTCTTCTTCAGAGAAATGACACAGGTGAAGCATGCTATGGAAGCAACCA	310
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Qy	311	TTGTACTCAGTAGGAGTATCAGTTTCTGATCGCTACTTCAAGGGTACTTTTTAGAAC	370
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AUTHORS Bloecker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.			
TITLE Direct Submission			
JOURNAL Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764			
COMMENT			
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.			
This clone (DKFP45101715) is available at the RZPD in Berlin.. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.			
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AC144439
VERSION
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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ORGANISM
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 39694)
Waterston.R.H.
Direct Submission
Submitted (16-APR-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
----- Project Information -----
Center project name: H_AA087042G10
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 39167 bases at least Q40
Consensus quality: 39319 bases at least Q30
Consensus quality: 39366 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 7028: contig of 7028 bp in length
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Qy 372 AAAGACTATCGGTGGTCCATGTCAAGTATGATGTTCAAGTGGGAGACTCATCTCAACC 431
Db 32736 AAAGACTATCGGTGGTCCATGTCAAGTATGATGTTCAAGTGGGAGACTCATCTCAACC 32795
Qy 432 ACGATCAATAACCCCTTTAGAAAGGGAATTTATTATGACGATGACAAATTTGGATCCA 491
Db 32796 ACGATCAATAACCCCGTTAGAAAGTGAATTTGTTATTGACCATGGAATTTTGAATCCA 32855
Qy 492 CAATGGTCTGAAACTCTGGATTCTGGATGGCTGACATGTGACACTGAAATAAGATTACG 551
Db 32856 CAGTGGTGTGAACCTCTGGATTCTGCAATGGCTGCAATGTGACACTGAAATAAGATTACG 32915
Qy 552 TTTGCATTATTTCTGAAAAACCTCTGTCATTAATCAACGAAGAAAAATTTAAAAATCTAG 611
Db 32916 ATTGCATTATTTCTGAAAAACCTCTGTCATTAATCAACGAAGAAAAATTTAAAAATCTAG 32975
Qy 612 ATTTAGGTGAGCTGACACTAGAGGCTGGAGAGATGACGATGATAGGTATCTCC 671
Db 32976 ATTTAGGTGAGCTGACACTAGAGGCTGGAGAGATGATAGGTATCTCC 33035
Qy 672 CACTGTACTCCACAAATGTCCAATAGCTTGGAGATATCTTTAATAAGCGCAATAGATT 731
Db 33036 CACTGTACTCCACAAATGTCCAATAGCTTGGAGATATCTTTAATAAGCGCAATAGATT 33095
Qy 732 CAAGTGCAGGCATTTACAGCCGGAGTGTGGTTATGGCTTGCAGCCGTGATCGTTGGACAGA 791
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Db 33096 C C A G T G C A G G C A T T C A C A G C T G G A G T G T G T A T G C C T T A C A G T C T G A T C T G T T G G A C A G A 33155
Qy 792 G T A C A G C A T A C A G A C G A T G G A A C C A G A T A A C C T G G A A C T A A T C T T T G A T T T T T T C G A A G A 851
Db 33156 G T A C A G C A T A C A G A C A A T G G A C C A G A T A A C C T G G A A C T A A T C T T T G A T T T T T T G A A G A 33215
Qy 852 A G A T C T C A G T G A G C A C G T A G T T C A G G G T G A T G C C C T T C C T T G G A C A T G T G G G T A C A G C T T G 911
Db 33216 A G A T C T C A G T G A G C A C A T A G T T C A A G G T G A T G C C C T C C C T G G A T G T G T G G G T A C A G C T T G 33275
Qy 912 T C T C T T A T C A T C C A C C A T T G T G A G A G T G G A A G A G T C T G G A A T T C T T A C T C T T C C C A T 971
Db 33276 T C T C T T A T C A T C C A C C A T T G T G A G A G T G G A A G A G T C T G G A A T T C T T A C T C T T C C C A T 33335
Qy 972 C A T G A G C A G A A T T C C G G A A A C A A T A G G C A A A G T G A G A T T G A C T A T A T A T A T T A A 1031
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Qy 1032 G C C A T T A C C A G G A T A C A G T T G T G A C A T G A A A T C T T C A T T T T C C A A G T A T T G G A A G C C A A G 1091
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Qy 1092 A A T A C C A T T G G A T T G T G C C A T C A G A G T G C A G G A A C T C T A C A C A A C T G C C A G C T G G C 1151
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Db 33512 T A - - - - - A A G A A A A T A C T A T T G C T T C T T A A G A A A T G C T C T A G T C A C G T G C A G C T T 33565
Qy 1212 T G T A G A A T T G A C G T A C A C C T T T C A A G G A C T T T G T G C C G T G G T A T A T C A T A T C T T A C 1271
Db 33566 T G T A G A A T T G A T G A C A C C T T T C A A G A G A C T T T G T G C C C A T G T A T A T C A T G A T C T T A C 33625
Qy 1272 C T G T T G T T T G A C T A T G A A A A A A A T T G A T G C T G A T C C A G T T G A A T T A T T T G A A A T T C C 1331
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Qy 1332 A G T - A A A G A A T T A C A T T T G A C C A A C C A G T T G T T A A G C T A C T C A T G T G A C T G C A C 1390
Db 33686 A G T A A A A A A A T T A A C A T T T G A C C A C T C C A G T T G T T A A A G C T A C T C A T G T G A C T G C A C 33745
Qy 1391 T G A A T C T A A G A T C G G A A A G A A T C T G T G T T C A G G A G A A A A T T C C T T T C A G A A A A T C 1450
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Qy 1451 A G C A A T T C C T T C T C T T A A G A T G G T T T A G A G T C T T T G C C A G A A G A T G T A G G T T T A A C A 1510
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Qy 1511 T T G A A T A A A A T G G A T C T C C A G C A A A G G A T G G A A T G T G G A T G T A A C T T T A C A C A T 1570
Db 33866 T T G A A T A A A A T G G A T C T C C A G C A A A G G A T G G A A T G T G G A T G T A A C A T T A C A C A T 33925
Qy 1571 A T T T T C A C A T G A A T C T G T T T T T G A T A T A A T T T A A A A A C T G T T T A G A A A A T T C T G G G A 1630
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Qy 1631 A G A G A G A A T A G T G T T T C T T C A T T T G A T G C A G A T A T T T G C A A T G T T G C A A G T T C G G A A A A G C 1690
Db 33986 A G A - G A G A T A G T G T T T C T T C A T T T G A T G C A G A T A T T T G C A C A A T G T T T G C C A A A G C 34044
Qy 1691 A G A C A A A T A T C C G A T A C T A T T T T T A C T C A A G G A A A A C T G A G A T T T A T C T G A A C T C A 1750
Db 34045 A G A C A A A T A T C C C A T A T T A T T T T T A A C T G A A G G A A A A C T G A G A T T T A T C T G A A C T C A 34104
Qy 1751 T G A C C T C A G A T C T C G A C A A C C C C A T T G C A A T G A G C T T T G C A C A G T T T G A A A A T C T A C 1810
Db 34105 T G A C C T C A G A T C T C G A C A A C C C C A T T G C A A T G A G C T T T G C A C A G T T T G A A A A T C T A C 34164
Qy 1811 T G G G G - - - - - 1815

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Qy 1816 - - - - - 1815
Db 34225 A G G T G G A T C A C C T G A G G T C A G A A G T T C A A G A T C A G C T T A G T C A A C A T G T G A A C C C A G 34284
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Db 34285 T C T C T A T A A T A T A C A A A A T T A G C T G G C A C C G T G T G G C A C C T G T A A T C C A G C T A 34344
Qy 1816 - - - - - 1815
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Db 34465 G A A A G A A A A A A T C T A C T G G A A A T A A T G T A C A T A C T G A A G A C T T G C T C A G A A A C C C A 34524
Qy 1852 T C C T A T A T T C A A G A G C A A A A G C T A A G G A C T A G T C A T A T T C T G C T G G G T G A T A C C 1911
Db 34525 T C C T A T A T T C A A G A G C A A A A G C T A A G G A C T A A T C A T A T T C T G C T G G G T G A T A A A A G C 34584
Qy 1912 A A T G A T C C T G A A A C A G A A G A A A T T G A A G A A C T T G G A G T T A A T G G T C T A A T T A T T A T G A T 1971
Db 34585 A G T G A T C C T G A A A G A A G A A A A T T G A T G G A A C T T G G A G T T A A T G G T C T A T T A T T A T G A T 34644
Qy 1972 A G A T A T A T A T G A T T G G A T G C T G A A C A A C C A A A T A T A T T C C A A G T G G A G A A A T T G A A A G C 2031
Db 34645 A G A T A T A T A T G A T T G G A T G C T G A C A A - - - - - C C A A G T G G A G C A A C T G G A A T G C 34693
Qy 2032 C T G A A C A G A A T T G C C A G A G C T T A A G A G C T G T T G T G T C C C A C T G T T A G C C G C T T T G T 2091
Db 34694 C T G A A C A A G A A T T G C C A G A G T A A G G C T G T T G T G T C C C A C T G T T A G C C A C T T T G T 34753
Qy 2092 C C C T A T C T T T G T G T G G G A G C T G A T A T C C A T G T G A T G C C A A C G G C A A T T G A T A A C G T G 2151
Db 34754 C C C T A T C T T T G T G T G A G G C C T G A T C C C A T G T G G A T G C C A A T G G C A A T G A T A T G T G 34813
Qy 2152 G A G A A T C T T A G T T T T T A T T T T G C A C A G A G T C A T T T T G G G G G G T G C A C C G C T G T T C T G G 2211
Db 34814 G A G A A T C T T A G T T T T T A T T T T G C A C A G A G T C A T T T T G G G G C A T G C A C C G C T T C T G G 34873
Qy 2212 T A T T C A T T T T C A C T A C T G A G C A T T G T G A T C A T G C C T T T T G G G C T T C T C A G T C A A T G 2271
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Db 34934 A A C A A T A A T A A A G A T A T T A A C T C T T T C A T A G A T T C T T G C A A G A T A T G C T A T T A A T 34993
Qy 2332 A C T T G C C A G A T A A T T G C A G T C A G T C T T T A T A T A G T A G A A A A T T A T T G T T A G T A 2391
Db 34994 A C T T A G C C A G G T A A T T G C A G T C A G T C T T T A C A G T A G A A A A T G A T T G T T G G T A 35053
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Qy 2452 C A T A G C A C T T T G A A A T T A C T A T A T A A A T A G C T C A T A T T T A C A C T T A C A C C T T T C A T T 2511
Db 35110 C A T A G C A C T T T G A A A T T A A A T A T A T A A A T A G C T A T A - T T A C A C T T A C A C C T T T C G T T 35168
Qy 2512 G A T C A G C T C G A A A T C T T T A G C A C T T A A G A A A A T A G A T A T G C A T A T A T A C T G A C C A 2571
Db 35169 G A T C A G G T C G A A A T C T T T A G C A C T T A A G A A A A T A G A T A T G C G T A T A T A C T G A C C A 35228
Qy 2572 T G A A A A A A A T A A G T A C C T C A A A T G C A T T G C A T T G C A T T G C A T T G C A A C T G C A C A A T C 2631
Db 35229 T G G A A A A A A T A A G T A C C T C A A A T G C A T T G C A T T G C A T T G C A T T G C A A C T G C A C A A T C 35288

Qy	2632	TTTGTGCCATCTTTGTATATAGGTAATTTTTTACATGGTTGACATGCACAAACACATTT	2691
Db	35289	TTTGTGCTTCTTTGTATATAGGTAATTTTTTACATGGTTGACATGCACATAACAGCATTT	35348
Qy	2692	TCATTCAGTATGAACCTTGAGGCTGCTGCCATCTTTTCCACTTTAAACCAACACGCTGGAAG	2751
Db	35349	TCCTTCAGTATGAACCTTGAGGCTGCTGCCATCTTTTCCACTTTAAACCAACGCTGGAAG	35408
Qy	2752	GTGAACCTCGAAACTTTGTTTTCATAAACTCTTTCAAAGTTGTTTTACATCAATGTTAAAT	2811
Db	35409	GTGAACCTTGAAACTTTGTTTTCATAAACTCTTTCAAAGTTGTTTTACATCGATATTAAT	35468
Qy	2812	TTCAAATGCTGCAGGGTAATTTTAATGTTATAAATAATTAAGTAAGAAAAAGTATGATTGC	2871
Db	35469	TTCAAGATGCTGCAGGGTAATTTTAATGTTATAAATAATTAAGTAAGAAAAAGTATGATTGC	35528
Qy	2872	ATACTTAGTAGATAGATCACACATACAAATCTCAATTCAGTGCATCTTTAGGTTGTTAA	2931
Db	35529	ATACTTAGTAGAATAGATCACACATATAAATCTCAATTCAGTGCATCTTTAACTGTTAA	35588
Qy	2932	GCATGAGATTTGACATGTTTACTTGTAGTTCCTTGTCATCTGTGGTGTAGGTGAGTATGA	2991
Db	35589	GCATGAGTTGTACATGTTTACTTGTAGTTCCTTGTCATCTGTGGTGTAGGTGAGTATGA	35648
Qy	2992	GAAGATGTCAGGACTGGACGTATTTTGTGCTCAAAAAAAGCGCTGTTTGTAGGCGT	3051
Db	35649	GAAGATGTCAGGACTGGACATATTTTGTGCTCAAAAAAAGCGCTGTTTGTAGGCGT	35704
Qy	3052	TTTAAATATGCTTATTTTGTGTGCTCTCACTACCTATTACACACTGTGCTTTGGGT	3111
Db	35705	TTTAAATATGCTTATTTTGTGTG- -TCTCACTACCTATTACACACTGTGCTTTGGGT	35762
Qy	3112	TTCTTTTGTATGCTGTGTGTTATACAGTAGTTAAATTTCCATGCAGAAAAATAAATGTC	3171
Db	35763	TT- -TTTGTGTATGTGTGCTGGAACAGTAGTTAAATTTCCATGCAGAAAAATAAATGTA	35821
Qy	3172	CTGAATTTCTCAA	3184
Db	35822	CTGAATTTCTCAT	35834
RESULT 11			
AC099654/c			
LOCUS	149259 bp DNA linear PRI 08-OCT-2003		
DEFINITION	Homo sapiens BAC clone RP11-1217F2 from 7, complete sequence.		
ACCESSION	AC099654		
VERSION	AC099654.5 GI:20146842		
KEYWORDS	HTG.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	Sulston,J.E. and Wilson,R.		
AUTHORS	Toward a complete human genome sequence		
JOURNAL	Genome Res. 8 (11), 1097-1108 (1998)		
MEDLINE	95063792		
PUBMED	9847074		
REFERENCE	2 (bases 1 to 149259)		
AUTHORS	Dignan,G., Kozlowski,A. and Swearingen-Shahid,S.		
TITLE	The sequence of Homo sapiens BAC clone RP11-1217F2		
JOURNAL	Unpublished (2001)		
REFERENCE	3 (bases 1 to 149259)		
AUTHORS	Waterston,R.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2001) Genome Sequencing Center, Washington		
University School of Medicine, 444 Forest Park Parkway, St. Louis,			
MO 63108, USA			
REFERENCE	4 (bases 1 to 149259)		
AUTHORS	Waterston,R.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (28-MAR-2002) Genome Sequencing Center, Washington		

QY 612 ATTTAGGGTGAAGCTGACACTAGAGGCTTGAGGGAAGATGACGATGATAGGGTATCTCC 671
Db 22565 ATTTAGGGTGAAGCTGACACTAGAGGCTTGAGGGAAGATGAGGATGATAGGGTATCTCC 22506
QY 672 CACTGTACTCCACAAATCTCCAAATAGCTTGGAGATATCTTAAATAGCGACAATGAGTT 731
Db 22505 CACTGTACTCCAAATCTCCAAATAGCATGAGATATCTTAAATATGTCACATGAGTT 22446
QY 732 CAAAGTCAGGCAATTCACAGCGGAGTGTGGTTATGGCTTGACGCTGATCGTTGGACAGA 791
Db 22445 CCAGTGCAGCAATTCACAGCTGGAGTGTGGTTATGGCTTGACAGTCTGATCGTTGGACAGA 22386
QY 792 GTACAGCATACAGACGATGGAACCGAGATAACCTGGAACTAACTTTTGTGATTTTTCGAAGA 851
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QY 852 AGATCTCAGTGAGCAGTGTAGTTACAGGGTGCATGCCCTTCTCGACATGTGGGTACAGCTTG 911
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Db 22265 TCTCTTATCATCCACCAATTCGTCGAGAGTGGAAAGAGTGTGGAAATCTTACTCTTCCCAT 22206
QY 972 CATGAGCAGAAATCCCGGAAAACAATAGGCAAAAGTGAGAGTTGACTATATATTAATTA 1031
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Db 22145 GCCATTGCGAGATACAGTTGTGACATGAATCTTCAATTTTCC-AGTATTTGAAGCCAG 22087
QY 1092 AATACATTGGAGTGTGGCCATCGAGTGCAGAAACTCTACAACTGCCCAGCTGCG 1151
Db 22086 AATACATTGGAGTGTGGCCATCGAGTGTGGAAACGCT---ACAACTGCCAGCTGCG 22030
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Db 22029 TA-----AAGAAATACTATTGCTTTTAAAGAAATGCTGTAGTCAATGTCGAGCCTT 21976
QY 1212 TGTAGAAATTTGAGTACACTTTCAAGGACTTTGTGCCGTGGTATATCATGATCTTAC 1271
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QY 1272 CTGTTGTTTGAATGATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTTCC 1331
Db 21915 CTGTTGTTTGAATGATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTTCC 21856
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Db 21735 AGCCATTTCTCTTAAAGATGTTTAAAGTCTTTTGCAGAGATGAGGGTTTAAACA 21676
QY 1511 TTGAAATTAATGATCTGCCAGCAAGGATGGAATGTGGATGGTAACTTTATCAACAT 1570
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QY 1571 ATTTGACATGAATCTGTTTGGATATAATTTTAAAACTGTTTGAAGAAATCTCGGA 1630
Db 21615 ATTTTGGCATGAATCTGTTTGGATATAATTTTAAAACTGTTTGAAGAAATCTCGGA 21556
QY 1631 ACAGAGATAGTGTCTCTCATTTGATGACAGATATTTGCAATGTTGCGCAAGC 1690
Db 21555 AGA-GAGAAATGTTTCTTCTCATTTGATGACAGATATTTGCAATGTTGCGCAAGC 21497

QY 1691 AGAACAAATATCCGATACATATTTTAACTCAAGGAAATCTGAGATTTATCTCTGAATCA 1750
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QY 1811 TGGGG----- 1815
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Db 21076 GAAAGAAAGAAATCTACTGGAATAAATGTACATCTGAAGACTTCTCAGAAACCA 21017
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QY 1972 AGGATATATGATGAGTCCCTGAAACCAATATATTTCCAGATGGAGCAATTTGAAACGC 2031
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QY 2032 CTGAAGCAGGAATTTCCAGAGCTTAAGAGCTTTGCTGCCACTTTGCTAGCCGCTTTGTT 2091
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QY 2092 CCCTCATCTTTGTGGGGAGTCTGATATCCATGTGGATGCCAACGGCAATTTGATAACGTC 2151
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QY 2152 GAGATGCTTATGTTTATTCGACAGAGTCAATTTTGGGGGCTGACCGCTGTTCTCGG 2211
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RESULT 14

BD156897

LOCUS 1803 bp DNA linear PAT 17-JAN-2003

DEFINITION Primer for synthesizing full-length cDNA and use thereof.

ACCESSION BD156897

VERSION BD156897.1 GI:27862655

KEYWORDS JP 2002191363-A/11740.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1803)

AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.

TITLE Primer for synthesizing full-length cDNA and use thereof

JOURNAL Patent: JP 2002191363-A 11740 09-JUL-2002;

COMMENT HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)

PN JP 2002191363-A/11740

PD 09-JUL-2002

PF 28-JUL-2000 JP 2000280990

PI TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU

PI SAITO,

PI JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,

PI KEIICHI NAGAI,TETSUJI OTSUKI

PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/PC 10,

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Primer for synthesizing full-length cDNA and use thereof FH Key

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SOURCE
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Db 61 TTTTCAGAAAAATCAGCCATTTCTTCTCTTAAGATGGTTTTAGAGTCTTTTGCAGAGATG 120
Qy 1499 TAGGGTTTAACTTGAATTAATTAAGATCTGCCAGCAAGGATGGAATGTTGGGATGTA 1558
Db 121 TAGGGTTTAACTTGAATTAATTAAGATCTGCCAGCAAGGATGGAATGTTGGGATGTA 180
Qy 1559 ACTTATCAACATATTTTGCATGATCTGTTTGGATATATATTTTAAAAAAGCTGTTTGTAG 1618
Db 181 ACTTATCAACATATTTTGCATGATCTGTTTGGATATATATTTTAAAAAAGCTGTTTGTAG 240
Qy 1619 AAAATTTCTGGGAAGGAGAGATAGTGTCTTCTCATTTGATGACAGATATTTGCACAATGG 1678
Db 241 AAAATTTCTGGGAAGGAGAGATAGTGTCTTCTCATTTGATGACAGATATTTGCACAATGG 300
Qy 1679 TTCGCAAAAGCAGACAAATATCCGATACCTATTTTAACTCAAGGAAAAATCTGAGATTT 1738
Db 301 TTCGCAAAAGCAGACAAATATCCGATACCTATTTTAACTCAAGGAAAAATCTGAGATTT 360

QY	1739	ATCCTGAACCTATGGACCTCAGATCTCGGACAACCCCAATGCAATGAGCTTTGCACAGT	1798
Db	361	ATCCTGAACCTATGGACCTCAGATCTCGGACAACCCCAATGCAATGAGCTTTGCACAGT	420
QY	1799	TTGAAATCTACTCGGGATAAATGTATACATCTGAGACTTCTCAGAAACCCCATCTTATA	1858
Db	421	TTGAAATCTACTCGGGATAAATGTATACATCTGAGACTTCTCAGAAACCCCATCTTATA	480
QY	1859	TTCAAGAGGAAAAGCTAAAGGACTAGTCAATCTCTGGGTGATGATACCAATGATC	1918
Db	481	TTCAAGAGGAAAAGCTAAAGGACTAGTCAATCTCTGGGTGATGATACCAATGATC	540
QY	1919	CTGAAAACAGAAAGAAATTTGAAGAACTTGGAGTTAATGTCTAATTTATGATAGATAT	1978
Db	541	CTGAAAACAGAAAGAAATTTGAAGAACTTGGAGTTAATGTCTAATTTATGATAGATAT	600
QY	1979	ATGATTGGATCGCTGAACCAAAATATATTTCCAAAGTGGAGCAATTTGGAACGCTGAAGC	2038
Db	601	ATGATTGGATCGCTGAACCAAAATATATTTCCAAAGTGGAGCAATTTGGAACGCTGAAGC	660
QY	2039	AGGAATTCGAGAGCTTAAGAGCTTTGTGTCCCACTGTTAGCGCTTTGTTCCTCAT	2098
Db	661	AGGAATTCGAGAGCTTAAGAGCTTTGTGTCCCACTGTTAGCGCTTTGTTCCTCAT	720
QY	2099	CTTTGTGGGAGTCTGATATCCATGTGGATGCCAAGCGCATTTGATGAGAGAAATG	2158
Db	721	CTTTGTGGGAGTCTGATATCCATGTGGATGCCAAGCGCATTTGATGAGAGAAATG	780
QY	2159	CTTACTTTTATATGACAGAGTCAATTTGGGGGGTGCACCGCTGTCTGGGTATTCAT	2218
Db	781	CTTACTTTTATATGACAGAGTCAATTTGGGGGGTGCACCGCTGTCTGGGTATTCAT	840
QY	2219	TTTTTCATCTGAGCATTTGTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAAT	2278
Db	841	TTTTTCATCTGAGCATTTGTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAAT	900
QY	2279	AATGAAGTATTTAACTCTTTTCACTACAGTTCTTGCAAGTATGCTAATTTAAATTA	2338
Db	901	AATGAAGTATTTAACTCTTTTCACTACAGTTCTTGCAAGTATGCTAATTTAAATTA	960
QY	2339	CAGGTATAATGCCAGTCACTCTTTATAGTGAGAAAATTTATTTGGTTAGTATATAA	2398
Db	961	CAGGTATAATGCCAGTCACTCTTTATAGTGAGAAAATTTATTTGGTTAGTATATAA	1020
QY	2399	TATTTTAACTAAATATATAATCTATAATTTAAACATATGTTTCAATTAAGCATAGCA	2458
Db	1021	TATTTTAACTAAATATATAATCTATAATTTAAACATATGTTTCAATTAAGCATAGCA	1080
QY	2459	CTTTGAAATTAACATATAAATAGCTCATATTTACATTTACAGCTTTTCATTTGATCAGG	2518
Db	1081	CTTTGAAATTAACATATAAATAGCTCATATTTACATTTACAGCTTTTCATTTGATCAGG	1140
QY	2519	TCGAAATCTTTAGCACTTAAGAAAATGACATATGCAATTTATACCTGACCATGAAAA	2578
Db	1141	TCGAAATCTTTAGCACTTAAGAAAATGACATATGCAATTTATACCTGACCATGAAAA	1200
QY	2579	AATAAGTACCTCAATGCAATTTGCACTGCTGATTCCACTGCACAAATCTTTGTGC	2638
Db	1201	AATAAGTACCTCAATGCAATTTGCACTGCTGATTCCACTGCACAAATCTTTGTGC	1260
QY	2639	CATCTTTGATATAGGTATTTTATCATGGTTGACATGACACCAACCATTTTCATTTCA	2698
Db	1261	CATCTTTGATATAGGTATTTTATCATGGTTGACATGACACCAACCATTTTCATTTCA	1320
QY	2699	GTATGAACCTTGAGGCTGCTGCAATTTTCCACTTAACCAACCGCCCTGAAGTGAACC	2758
Db	1321	GTATGAACCTTGAGGCTGCTGCAATTTTCCACTTAACCAACCGCCCTGAAGTGAACC	1380
QY	2759	TCGAACTTTGTCATATAATCTTTCAAAAGTCTTTTACATCAATGTTTAAATTTTCAAAA	2818
Db	1381	TCGAACTTTGTCATATAATCTTTCAAAAGTCTTTTACATCAATGTTTAAATTTTCAAAA	1440

QY	2819	TGCTGCAGGGTAATTTAATGTATATAAATATTTAGTAAGAAAAAGTATGTATTGCTACTTA	2878
Db	1441	TGCTGCAGGGTAATTTAATGTATATAAATATTTAGTAAGAAAAAGTATGTATTGCTACTTA	1500
QY	2879	GTAGAATAGATCAACAACATACAAATTTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAG	2938
Db	1501	GTAGAATAGATCAACAACATACAAATTTCAATTCAGTGCATGCTTTAGGTGTTAAGCATGAG	1560
QY	2939	ATTGTACATGTTTACTGTTAGTCTCTTGCATCTGTGGTGTAGGTGAGTATGAGAAGATG	2998
Db	1561	ATTGTACATGTTTACTGTTAGTCTCTTGCATCTGTGGTGTAGGTGAGTATGAGAAGATG	1620
QY	2999	TCAAGGACTTGGACGTATTTTGTTCCTAAAAAAGGCTGTTTGTAGGCGTTTAAAAAT	3058
Db	1621	TCAAGGACTTGGACGTATTTTGTTCCTAAAAAAGGCTGTTTGTAGGCGTTTAAAAAT	1680
QY	3059	ATGCTTATTTTGTGTGCTCTCCTACCTATTTACACATGTTGCTTCTGCGGTTTGTGTTT	3118
Db	1681	ATGCTTATTTTGTGTGCTCTCCTACCTATTTACACATGTTGCTTCTGCGGTTTGTGTTT	1740
QY	3119	GTATGCGGTGTTTATACAGTAGTTAAATTTCCATGCAGAAAAATAAATGTCCTGAATT	3178
Db	1741	GTATGCGGTGTTTATACAGTAGTTAAATTTCCATGCAGAAAAATAAATGTCCTGAATT	1800
QY	3179	CTC 3181	
Db	1801	CTC 1803	

Search completed: July 2, 2005, 16:56:09
Job time : 13678 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 2, 2005, 16:56:17 ; Search time 1861 Seconds
(without alignments)
10805.278 Million cell updates/sec

Title: US-10-047-855-4
Perfect score: 3206
Sequence: 1 gtcacccacgcgtccggc.....aaaaaaagcgccgcgc 3206

Scoring table: IDENTITY NUC
Gap 10.0 , Gapext 1.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
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- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
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- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
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- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3206	100.0	3206	16	US-10-047-855-4
2	3206	100.0	3206	17	US-10-426-776-34
3	3178	99.1	3265	21	US-10-887-553A-1007
4	3166	98.8	3499	10	US-09-814-353-21000
5	3164.4	98.7	3499	20	US-10-357-930-23730
6	3164.4	98.7	3499	20	US-10-357-930-29632
7	2481.8	77.4	2738	17	US-10-426-776-32

8	2019	63.0	2019	21	US-10-772-636-25	Sequence 25, Appl
9	1471.2	45.9	3381	17	US-10-426-776-39	Sequence 39, Appl
10	991	30.9	2393	17	US-10-426-776-48	Sequence 48, Appl
11	522.4	16.3	524	9	US-09-796-692-4214	Sequence 4214, Ap
12	522.4	16.3	524	14	US-10-040-862-4214	Sequence 4214, Ap
13	522.4	16.3	524	17	US-10-057-475B-4214	Sequence 4214, Ap
14	522.4	16.3	524	17	US-10-154-884B-4214	Sequence 4214, Ap
15	522.4	16.3	524	19	US-10-764-324-4214	Sequence 4214, Ap
16	486.4	15.2	546	9	US-09-777-564-71	Sequence 71, Appl
17	486.4	15.2	546	14	US-10-015-219-71	Sequence 71, Appl
18	469.4	14.6	471	9	US-09-998-598-1849	Sequence 1849, Ap
19	427	13.3	427	10	US-09-918-995-6192	Sequence 1692, Ap
20	414.8	12.9	520	10	US-09-814-353-16669	Sequence 16669, A
21	413.8	12.9	436	9	US-09-796-692-8067	Sequence 8067, Ap
22	413.8	12.9	436	14	US-10-040-862-8067	Sequence 8067, Ap
23	413.8	12.9	436	17	US-10-057-475B-8067	Sequence 8067, Ap
24	413.8	12.9	436	17	US-10-154-884B-8067	Sequence 8067, Ap
25	413.8	12.9	436	19	US-10-764-324-8067	Sequence 8067, Ap
C 26	365.6	11.4	403	9	US-09-777-564-183	Sequence 183, App
C 27	365.6	11.4	403	14	US-10-015-219-183	Sequence 183, App
28	363.4	11.3	396	10	US-09-814-353-3977	Sequence 3977, Ap
29	363.4	11.3	396	10	US-09-814-353-10285	Sequence 10285, A
30	326.6	10.2	425	20	US-10-357-930-35883	Sequence 35883, A
31	326.6	10.2	425	20	US-10-357-930-44946	Sequence 44946, A
C 33	296.4	9.2	478	9	US-09-867-701-2369	Sequence 2369, Ap
C 34	291	9.1	510	9	US-09-867-701-2369	Sequence 2369, Ap
35	271	8.5	359	20	US-10-357-930-5885	Sequence 5885, Ap
36	208.4	6.5	463	9	US-09-864-761-2380	Sequence 2380, Ap
37	193	6.0	193	9	US-09-864-761-31997	Sequence 31997, A
38	185.8	5.8	1121	14	US-10-198-846-11446	Sequence 11446, A
39	166	5.2	401	9	US-09-864-761-15483	Sequence 15483, A
40	163.4	5.1	323	9	US-09-728-445-622	Sequence 622, App
41	151	4.7	151	9	US-09-864-761-19114	Sequence 19114, A
42	138	4.3	429	9	US-09-864-761-15673	Sequence 15673, A
43	122	3.8	122	9	US-09-864-761-32178	Sequence 32178, A
44	120.2	3.7	354	17	US-10-242-535A-35647	Sequence 35647, A
45	120.2	3.7	354	18	US-10-085-783A-35647	Sequence 35647, A

ALIGNMENTS

RESULT 1
US-10-047-855-4
; Sequence 4, Application US/10047855
; Publication No. US20030165863A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Lillian Wei-Ming
; TITLE OF INVENTION: NARC10 and NARC16, Programmed Cell
; DEATH-ASSOCIATED MOLECULES AND USES THEREOF
; FILE REFERENCE: 35800/242056
; CURRENT APPLICATION NUMBER: US/10/047,855
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,306
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3206
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)...(2163)
; NAME/KEY: misc feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: Vector sequence
US-10-047-855-4

Query Match 100.0%; Score 3206; DB 16; Length 3206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GTCGACCCACGCGTCCGGCGGAGGCA	CGGACGGCGGCGCCCGGTACCTCTGCCC	CGGCT	60
Db	1	GTCGACCCACGCGTCCGGCGGAGGCA	CGGACGGCGGCGCCCGGTACCTCTGCCC	CGGCT	60
QY	61	CCTCGCTCTCGGGGGGGCGGCGGAG	CGGACCTCGGACCTAGCGAAACCCGGAG	CACG	120
Db	61	CCTCGCTCTCGGGGGGGCGGCGGAG	CGGACCTCGGACCTAGCGAAACCCGGAG	CACG	120
QY	121	ACATCATAAATAAATCCATCAGAAAT	GACACCTTCTCAGGTTGGCTTTGAAATA	AGAGGA	180
Db	121	ACATCATAAATAAATCCATCAGAAAT	GACACCTTCTCAGGTTGGCTTTGAAATA	AGAGGA	180
QY	181	ACTCTTTTACCAGGAGAAAGTTTTT	GGCATATGTGGAAGCTGTGATCTTTGG	GGAACCTG	240
Db	181	ACTCTTTTACCAGGAGAAAGTTTTT	GGCATATGTGGAAGCTGTGATCTTTGG	GGAACCTG	240
QY	241	AATCCTCAAAATGTGTGGCTCTTCT	TCCAGAGAAATGACACAGGTGAAAGCT	ATATGG	300
Db	241	AATCCTCAAAATGTGTGGCTCTTCT	TCCAGAGAAATGACACAGGTGAAAGCT	ATATGG	300
QY	301	AAAGCAACATGTACTCAGTAGAGGAT	ATCAGTTCAAGTATCGTACTTCAAAGG	GTAC	360
Db	301	AAAGCAACATGTACTCAGTAGAGGAT	ATCAGTTCAAGTATCGTACTTCAAAGG	GTAC	360
QY	361	TTTTTTAGAACCAAGACATATCGGT	GGTCCATGTCAAGTGATGTTCACAA	GTGGAGACT	420
Db	361	TTTTTTAGAACCAAGACATATCGGT	GGTCCATGTCAAGTGATGTTCACAA	GTGGAGACT	420
QY	421	CATCTACACCAACGATCAATAACCC	CTTTAGAAAGCGAAATATATTTAG	CGATGGACAA	480
Db	421	CATCTACACCAACGATCAATAACCC	CTTTAGAAAGCGAAATATATTTAG	CGATGGACAA	480
QY	481	TTTTGGAATCCCAATGTGTGAAACT	CTGGAATCTGGATCGCTGACATGT	CAGACTGAA	540
Db	481	TTTTGGAATCCCAATGTGTGAAACT	CTGGAATCTGGATCGCTGACATGT	CAGACTGAA	540
QY	541	ATAAGATTACGTTTGCAATTAITCT	GAAAAACCTCCTGTGCAATAACCA	AGAAAAATTA	600
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QY	601	AAAAATCTAGATTAGGTGAACTGAC	TAGAACGCTGGAGGAGATGACGAT	GAT	660
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QY	661	AGGTTATCTCCCACTGATCTCCACA	AAATGTCCAAATAGCTTGAATATCT	TAAATAGC	720
Db	661	AGGTTATCTCCCACTGATCTCCACA	AAATGTCCAAATAGCTTGAATATCT	TAAATAGC	720
QY	721	GACATGAGTTCAAGTGCAGGCAIT	CACAGCCGAGTGTGTTATGGCTT	GACGCTGAT	780
Db	721	GACATGAGTTCAAGTGCAGGCAIT	CACAGCCGAGTGTGTTATGGCTT	GACGCTGAT	780
QY	781	CGTTGGACAGAGTACAGCATACAG	AGTGGAAACCGATTAATCTTTGAT		840
Db	781	CGTTGGACAGAGTACAGCATACAG	AGTGGAAACCGATTAATCTTTGAT		840
QY	841	TTTTTTCGAAAGATCTCAGTGAGCA	GTAGTTTCAGGTTGATCCCTCGACA	TATG	900
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QY	901	GGTACAGCTTGTCTTATCATCCAC	CAATGTCTGAGAGTGGAAAGTCT	CGAAATCTT	960
Db	901	GGTACAGCTTGTCTTATCATCCCA	ATTTGCTGAGAGTGGAAAGTCT	CGAAATCTT	960
QY	961	ACTCTTTCCCATATGAGCAAAAT	CTCCGGAAAAAATAGGCGAAAGT	GTGACTAT	1020
Db	961	ACTCTTTCCCATATGAGCAAAAT	CTCCGGAAAAAATAGGCGAAAGT	GTGACTAT	1020
QY	1021	ATAATTTAAGCCATTACAGAGAT	CAGTTGTGACATGAATCTTCA	TTTTTCCAGTAT	1080
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QY	1081	TGGAAGCCAAAGTAATACCATTTGG	CCATCGAGTGCAGGAAAATCTTACA	CAACT	1140
Db	1081	TGGAAGCCAAAGTAATACCATTTGG	CCATCGAGTGCAGGAAAATCTTACA	CAACT	1140
QY	1141	GCCAGCTGGCTAAAGTTCAAGAAAT	ACTATTTGCTTTTAAAGAAATGCT	GTAGTCAAT	1200
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QY	1201	GGTGAGCCCTTTGTAGAATTTGAC	GTACACCTTTCAAAGGACTTTTGT	CCCGTGTATAT	1260
Db	1201	GGTGAGCCCTTTGTAGAATTTGAC	GTACACCTTTCAAAGGACTTTTGT	CCCGTGTATAT	1260
QY	1261	CATGATCTTACCTGTTGTTGACTAT	GAAAAAGAAATTTGATGCTGAT	CCAGTTGAATTA	1320
Db	1261	CATGATCTTACCTGTTGTTGACTAT	GAAAAAGAAATTTGATGCTGAT	CCAGTTGAATTA	1320
QY	1321	TTTTGAAATTCAGTAAAAAGAAATTA	CAATTTGACCAACTCCAGTTGTT	TAAGCTCACTCAT	1380
Db	1321	TTTTGAAATTCAGTAAAAAGAAATTA	CAATTTGACCAACTCCAGTTGTT	TAAGCTCACTCAT	1380
QY	1381	GTGACTGCACTGAAATCTAAGGAT	CGGAAAGAAATCTGTGGTTCA	GAGGAAAAATTCCTTT	1440
Db	1381	GTGACTGCACTGAAATCTAAGGAT	CGGAAAGAAATCTGTGGTTCA	GAGGAAAAATTCCTTT	1440
QY	1441	TCAGAAAAATCAGCCATTTCTTCT	TAAAGATGTTTTAGAGTCTTTG	CCAGAAGATGTA	1500
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Db	1501	GGGTTTTAAATCAATTAATAAAT	TGGATCTCCAGCAAGGATGGAAT	GTGGATGGTAAC	1560
QY	1561	TTATCAACATATTTTGCACATGAAT	CTGTTTTTGGATATAATTTTAA	AAAACTGTTTTAGAA	1620
Db	1561	TTATCAACATATTTTGCACATGAAT	CTGTTTTTGGATATAATTTTAA	AAAACTGTTTTAGAA	1620
QY	1621	AATTTCTGGGAAGGAGAGAAATAG	TGTTTTCTTCAATTTGATGCAGAT	ATTTTGCAATGGTT	1680
Db	1621	AATTTCTGGGAAGGAGAGAAATAG	TGTTTTCTTCAATTTGATGCAGAT	ATTTTGCAATGGTT	1680
QY	1681	CGGCAAAAGCAGAAACAAATATCC	GATACATATTTTAACTCAAGGAA	AAATCTGAGATTTAT	1740
Db	1681	CGGCAAAAGCAGAAACAAATATCC	GATACATATTTTAACTCAAGGAA	AAATCTGAGATTTAT	1740
QY	1741	CCTGAATCTATGACCTCAGATCTCG	GAACCCCATTTGCAATGAGCTTTG	CACAGTTT	1800
Db	1741	CCTGAATCTATGACCTCAGATCTCG	GAACCCCATTTGCAATGAGCTTTG	CACAGTTT	1800
QY	1801	GAAAACTCTACTGGGATATAATGT	ACATCTGAAAGACTTGTCTCAGAA	ACCCCATCTATATTT	1860
Db	1801	GAAAACTCTACTGGGATATAATGT	ACATCTGAAAGACTTGTCTCAGAA	ACCCCATCTATATTT	1860
QY	1861	CAAGAGCAAAAGCTAAGGACTAGT	CATATTTCTGTGGGGTGATGAT	CAATGATCCT	1920
Db	1861	CAAGAGCAAAAGCTAAGGACTAGT	CATATTTCTGTGGGGTGATGAT	CAATGATCCT	1920
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QY	2041	GAAATGGCAGAGCTTAAAGAGCT	TTTGTGCCCATCTGTAGCCGCT	TTTGTCCCTCATCT	2100
Db	2041	GAAATGGCAGAGCTTAAAGAGCT	TTTGTGCCCATCTGTAGCCGCT	TTTGTCCCTCATCT	2100
QY	2101	TTGTGTGGGAGTCTGATATCCAT	GTGGATGCCAACCGCATTTGATA	ACGTGGAGAAATGCT	2160
Db	2101	TTGTGTGGGAGTCTGATATCCAT	GTGGATGCCAACCGCATTTGATA	ACGTGGAGAAATGCT	2160
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Db 2161 TAGTTTTTATGACAGAGGTCAATTTGGGGCGTGACCGTGTCTGGGTATTCATTT 2220
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Db 2221 TTTCATCAGTGCAGCATTTGTTGATCTATGCTTTTGGGCTTCTCAGTTCATTAAGCAATAA 2280
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US-10-426-776-34
; Sequence 34, Application US/10426776
; Publication No. US20040009553A1
; GENERAL INFORMATION:
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; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SC1, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; FILE REFERENCE: MPI03-0620MINIM
; CURRENT APPLICATION NUMBER: US/10/426,776
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229,662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795,691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105,992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406,045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314,881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161,188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3206
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-426-776-34

Query Match 100.0%; Score 3206; DB 17; Length 3206;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 ACATCAATAAATAATTCATCAGATGACCTTCTCAGGTTGCTTTGAATAAAGAGA 180
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Db 1939 AAGCTAAGGACATGATCATATTCGTCTGGGTGATGATACCAATGATCCTGAAACAGAA 1998
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Qy	1871	AAGCTAAGGAGTAGTCAATATTCCTGGGGTGATGATACCAATGATCTCTGAAAAACAGAA	1930
Db	1947	AAGCTAAGGAGTAGTCAATATTCCTGGGGTGATGATACCAATGATCTCTGAAAAACAGAA	2006
Qy	1931	GGAAATTTGAAGGAACCTTGGAGTTAATCGTCTAAATTTATGATAGGATATATGATTTGATGC	1990
Db	2007	GGAAATTTGAAGGAACCTTGGAGTTAATCGTCTAAATTTATGATAGGATATATGATTTGATGC	2066
Qy	1991	CTGAAACAAACCAATATATTTCCAAGTGAGCAATTTGGAACGCTTGAGCAGGAATTCGCAG	2050
Db	2067	CTGAAACAAACCAATATATTTCCAAGTGAGCAATTTGGAACGCTTGAGCAGGAATTCGCAG	2126
Qy	2051	AGCTTAAGAGCTGTTTGTGCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2110
Db	2127	AGCTTAAGAGCTGTTTGTGCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGG	2186
Qy	2111	AGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTTGGAGAAATGCTTAGTTTTAT	2170
Db	2187	AGTCTGATATCCATGTGGATGCCAACGGCATTTGATAACGTTGGAGAAATGCTTAGTTTTAT	2246
Qy	2171	TGCAACAGAGTTCATTTTGGGGGGCGTGACCGCTGTTCTGGGTATTCATTTTTTCACTAC	2230
Db	2247	TGCAACAGAGTTCATTTTGGGGGGCGTGACCGCTGTTCTGGGTATTCATTTTTTCACTAC	2306
Qy	2231	AGCAATGTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTT	2290
Db	2307	AGCAATGTTGATCTATGCTTTTGGGCTTCTCAGTTCAATGAAGCAATAATGAAGTATTTT	2366
Qy	2291	AACTCTTTTCACTACAGTTCTTTGCAAGTATGCTATTTAAATTTACTTTGCCAGGTATAATG	2350
Db	2367	AACTCTTTTCACTACAGTTCTTTGCAAGTATGCTATTTAAATTTACTTTGCCAGGTATAATG	2426
Qy	2351	CCAGTCAGTCTCTTTATAGTGAGAAAAATTTAATGGTTAGTAATAATAATAATTTTAAACTA	2410
Db	2427	CCAGTCAGTCTCTTTATAGTGAGAAAAATTTAATGGTTAGTAATAATAATAATTTTAAACTA	2486
Qy	2411	AAATATAAAATCTATAATGTTTAAACATATGTTTCAATTAAGCATAGCACTTTTGAATATAA	2470
Db	2487	AAATATAAAATCTATAATGTTTAAACATATGTTTCAATTAAGCATAGCACTTTTGAATATAA	2546
Qy	2471	CTATATAAATAGTCTCATATTTTACCTTACAGCTTTTTCATTTTGATCAGGCTCTGAAATCTTT	2530
Db	2547	CTATATAAATAGTCTCATATTTTACCTTACAGCTTTTTCATTTTGATCAGGCTCTGAAATCTTT	2606
Qy	2531	AGCACTTAAGGAAAAATGACTATGCATAATATATACCTGACCAATGAAAAAAAATAAGTACCTC	2590
Db	2607	AGCACTTAAGGAAAAATGACTATGCATAATATATACCTGACCAATGAAAAAAAATAAGTACCTC	2666

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RESULT 5
US-10-357-930-23730
; Sequence 23730, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23730

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: LENGTH: 3499
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 3497..3491
: OTHER INFORMATION: n = A,T,C or G
US-10-357-930-23730

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Query Match	98.7%	Score 3164.4;	DB 20;	Length 3493;
Best Local Similarity	99.8%	Pred. NO. 0;		
Matches 3168;	Conservative	0;	Mismatches 6;	Indels 0; Gaps 0;

Qy	11	CGCTCGGGGAGGACGAGCGGGGGGCCCGGTACTCTGC CGCGGTCTCGTCTC	70
Db	87	GAGCGCTGGCGAGGACGAGCGGGGGCCCGGTACCTCTGC CGCGGTCTCGTCTC	146
Qy	71	GGCGGGGGCGGCGAGCGGACCTCGGACTAGCNAACCGGAGGACGACATCATAA	130
Db	147	GGCGGGGGCGGCGAGCGGACCTCGGACTAGCNAACCGGAGGACGACATCATAA	206
Qy	131	ATAAATCCATCAGAATCACCTTCTCAGGTTGCTTTGAATAAGAGAACTCTTTTAC	190
Db	207	ATAAATCCATCAGAATGACACTTCTCAGGTTGCTTTGAATAAGAGAACTCTTTTAC	266
Qy	191	CAGSAGAA GTTTTTGCGATATGTGGAAGCTGTGATGCTTTTGGGAACTTGGAACTCCTCAA	250
Db	267	CAGSAGAA GTTTTTGCGATATGTGGAAGCTGTGATGCTTTTGGGAACTTGGAACTCCTCAA	326
Qy	251	ATGCTGTGGCTCTTCTTCAGAGAATGACACAGGTGAAGCATGCTATGGAAGCAACA	310
Db	327	ATGCTGTGGCTCTTCTTCAGAGAATGACACAGGTGAAGCATGCTATGGAAGCAACA	386
Qy	311	TTGTACTCAGTAGAGGAGTACAGTTCAGTATCGCTACTTCAAAGGGTACTTTTTAGAAC	370
Db	387	TTGTACTCAGTAGAGGAGTACAGTTCAGTATCGCTACTTCAAAGGGTACTTTTTAGAAC	446
Qy	371	CAAAGACTATCGGTGGTCCATGTCCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAC	430
Db	447	CAAAGACTATCGGTGGTCCATGTCCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAAC	506
Qy	431	CAGATCAATAA CCCCTTTAGAAAGCGAAATTATTATTGACGATGGACAAATTTGGAATCC	490
Db	507	CAGATCAATAA CCCCTTTAGAAAGCGAAATTATTATTGACGATGGACAAATTTGGAATCC	566
Qy	491	ACAATGGTGTGAAACTCTGATTTCTGATGGCTGACATGTCAGACTGAATAAGATTAC	550
Db	567	ACAATGGTGTGAAACTCTGATTTCTGATGGCTGACATGTCAGACTGAATAAGATTAC	626
Qy	551	GTTTGCAATTATCTGAAAAACCCTCTGTGTCATAA CCAAGAAAAAATTTAAAAAATCTA	610
Db	627	GTTTGCAATTATCTGAAAAACCCTCTGTGTCATAA CCAAGAAAAAATTTAAAAAATCTA	686
Qy	611	GATTTAGGCTGAAGCTGACACTAGAAGCCTGGAGGAAGATGACGATAGGGTATCTC	670
Db	687	GATTTAGGCTGAAGCTGACACTAGAAGCCTGGAGGAAGATGACGATAGGGTATCTC	746
Qy	671	CCACTGTCTCCAAAATGTCAAATAGCTTGGAGATATCCTTAATAGCGACATGAGT	730
Db	747	CCACTGTCTCCAAAATGTCAAATAGCTTGGAGATATCCTTAATAGCGACATGAGT	806
Qy	731	TCAAGTCGAGCATTCACAGCGGAGTGTGGTTATGGCTTCGAGCTGATCGTTGGACAG	790
Db	807	TCAAGTCGAGCATTCACAGCGGAGTGTGGTTATGGCTTCGAGCTGATCGTTGGACAG	866
Qy	791	AGTACAGCATACAGACGATGSAACCATTAACCTGGAACTAATCTTTTTCGAAG	850
Db	867	AGTACAGCATACAGACGATGSAACCATTAACCTGGAACTAATCTTTTTCGAAG	926
Qy	851	AAGATCTCAGTAGCAGTATGTCAGGGTGTATGCCCTTCTCGGACATGTGGGTACAGTT	910
Db	927	AAGATCTCAGTAGCAGTATGTCAGGGTGTATGCCCTTCTCGGACATGTGGGTACAGTT	986

Qy	911	GTCTCTTATCATCCACCAATTCCTGAGAGTGGAAAGAGTGTCTGGAATCTTCTACTCTTCCCCA	970
Db	987	GTCTCTTATCATCCACCAATTCCTGAGAGTGGAAAGAGTGTCTGGAATCTTCTACTCTTCCCCA	1046
Qy	971	TCATGACGAAATTCCTCCGAAAAACAATATGGCAAAAGTGAGAGTTGACTATATAATATTATTA	1030
Db	1047	TCATGACGAAATTCCTCCGAAAAACAATATGGCAAAAGTGAGAGTTGACTATATAATATTATTA	1106
Qy	1031	AGCCATTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCCAAAGTATTTGGAAGCCAA	1090
Db	1107	AGCCATTACAGGATACAGTTGTGACATGAAATCTTCAATTTTCCAAAGTATTTGGAAGCCAA	1166
Qy	1091	GAATACCAATGGAGTGTGGCCATCGAGGTGCAGGAAACTCTACAACAACTGCCCGAGCTGG	1150
Db	1167	GAATACCAATGGAGTGTGGCCATCGAGGTGCAGGAAACTCTACAACAACTGCCCGAGCTGG	1226
Qy	1151	CTAAAGTTCAAGAAATACATATTGCTTCTTTTAAGAAATGCTGCTAGTCACTGGTGCAGCCT	1210
Db	1227	CTAAAGTTCAAGAAATACATATTGCTTCTTTTAAGAAATGCTGCTAGTCACTGGTGCAGCCT	1286
Qy	1211	TTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTA	1270
Db	1287	TTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTA	1346
Qy	1271	CCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATAATTC	1330
Db	1347	CCTGTTGTTGACTATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATAATTC	1406
Qy	1331	CAGTAAAGAAATTAACAATTTTGACCACTCAGTTGTTTAAAGCTCACTCATGTGACTGAC	1390
Db	1407	CAGTAAAGAAATTTAAACATTTTGACCACTCAGTTGTTTAAAGCTCACTCATGTGACTGAC	1466
Qy	1391	TGAAATCTAAGGATCGGAAGAAATCTGTGTTTCAGGAGGAAAAATTCCTTTTCAGAAAAATC	1450
Db	1467	TGAAATCTAAGGATCGGAAGAAATCTGTGTTTCAGGAGGAAAAATTCCTTTTCAGAAAAATC	1526
Qy	1451	AGCCATTTCTCTCTTAAGATGGTTTGAAGTCTTTGCCAGAAAGATGTAGGGTTTAAACA	1510
Db	1527	AGCCATTTCTCTCTCTTAAGATGGTTTGAAGTCTTTGCCAGAAAGATGTAGGGTTTAAACA	1586
Qy	1511	TTGAAATAAAATCGATCTGCACCAAGGATGGGAATGGGAATGGTAACCTTATCAACAT	1570
Db	1587	TTGAAATAAAATCGATCTGCACCAAGGATGGGAATGGGAATGGTAACCTTATCAACAT	1646
Qy	1571	ATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAAAATCTGTTTTAGAAAAATCTCGGGA	1630
Db	1647	ATTTTGACATGAATCTGTTTTTGGATATAATTTTAAAAAATCTGTTTTAGAAAAATCTCGGGA	1706
Qy	1631	AGAGGAAATAGTGTGTTTTCTTCATTTTGATGACAGATATTTTGCACAATGGTTTCGGCAAAAGC	1690
Db	1707	AGAGGAAATAGTGTGTTTTCTTCATTTTGATGACAGATATTTTGCACAATGGTTTCGGCAAAAGC	1766
Qy	1691	AGAACAAATCCGATACATATTTTAACTTCAGGAAAACTGGAGATTATCCTGAACTCA	1750
Db	1767	AGAACAAATCCGATACATATTTTAACTTCAGGAAAACTGGAGATTATCCTGAACTCA	1826
Qy	1751	TGGACCTCAGATCTCGGACAAACCCCAATTTGCAATGAGCTTTGCACAGTTTGAATAATCTCAC	1810
Db	1827	TGGACCTCAGATCTCGGACAAACCCCAATTTGCAATGAGCTTTGCACAGTTTGAATAATCTCAC	1886
Qy	1811	TGGGGATAAATGTACATACCTGATGAAAGCTTGTCTCAGAAACCCCATCTATATTTCAAGAGCAA	1870
Db	1887	TGGGGATAAATGTACATACCTGATGAAAGCTTGTCTCAGAAACCCCATCTATATTTCAAGAGCAA	1946
Qy	1871	AAGCTAAGGACTAGTCAATATTTCTGCTGGGGTCAATGATACCAATGATCCTGAAAAACAGAA	1930
Db	1947	AAGCTAAGGACTAGTCAATATTTCTGCTGGGGTCAATGATACCAATGATCCTGAAAAACAGAA	2006
Qy	1931	GGAAATTTGAAGGAATTTGGAGTTTAAATGGTCTAATTTTATGATAGGATATATGATTTGATGC	1990
Db	2007	GGAAATTTGAAGGAATTTGGAGTTTAAATGGTCTAATTTTATGATAGGATATATGATTTGATGC	2066
Qy	1991	CTGAACCAACAAATATATTTCCAAAGTGGAGCAATTTGGAACGCCTCGAAGACGGAATTCGCCAG	2050

Db	2067	CTGAACCAACCAATATATTCCTCAAGTGAGACAAATGGAAACCGCTGAAGCAGGAATTCGCAG	2126
Qy	2051	AGCTTAAGAGCTGTTTGTGTCCTCACTGTTAGCCGCTTTTGTTCCTCATCTTTGTGTGGGG	2110
Db	2127	AGCTTAAGAGCTGTTTGTGTCCTCACTGTTAGCCGCTTTTGTTCCTCATCTTTGTGTGGGG	2186
Qy	2111	AGTCTGATATCCATGTGTGATGCCAACGGCAATGTATTAAGCTGGAGATGCTAGTTTAT	2170
Db	2187	AGTCTGATATCCATGTGTGATGCCAACGGCAATGTATTAAGCTGGAGATGCTAGTTTAT	2246
Qy	2171	TGCACAGAGCTCATTTTGGGGCGTGCACCGCTCTTCTGGGTATTCATTTTTCATCACTG	2230
Db	2247	TGCACAGAGCTCATTTTGGGGCGTGCACCGCTCTTCTGGGTATTCATTTTTCATCACTG	2306
Qy	2231	AGCATTTGTGATCTATGCTTTTGGGCTTCTCAGTTCATTAAGCAATAATGAAGTATTT	2290
Db	2307	AGCATTTGTGATCTATGCTTTTGGGCTTCTCAGTTCATTAAGCAATAATGAAGTATTT	2366
Qy	2291	AACCTCTTTCACCTACAGTTCTTTCAGAGTATGCTATTTAAATTACTTGGCCAGGTATTAATG	2350
Db	2367	AACCTCTTTCACCTACAGTTCTTTCAGAGTATGCTATTTAAATTACTTGGCCAGGTATTAATG	2426
Qy	2351	CCAGTCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTAAATAATAATTTTAAACTA	2410
Db	2427	CCAGTCAGTCTCTTTATAGTGAGAAAATTTATTTGGTTAGTAAATAATAATTTTAAACTA	2486
Qy	2411	ATATATAAATCTATAATGTTTAAACATATGTTTCAATTAAGCAATAGCACTTTGAAATTA	2470
Db	2487	ATATATAAATCTATAATGTTTAAACATATGTTTCAATTAAGCAATAGCACTTTGAAATTA	2546
Qy	2471	CTATATAAATAGCTCATATTTACCTTACAGCTTTTCAATTTGATCAGTCTGAAATCTTT	2530
Db	2547	CTATATAAATAGCTCATATTTACCTTACAGCTTTTCAATTTGATCAGTCTGAAATCTTT	2606
Qy	2531	AGCACTTAAGAAAATGACTATGCTAATTAATFACCTGACCATGAAGAAAATAAGTACCTC	2590
Db	2607	AGCACTTAAGAAAATGACTATGCTAATTAATFACCTGACCATGAAGAAAATAAGTACCTC	2666
Qy	2591	AAATGATCATTTGTCACCTGATTTTCCAACTGCAACAACTTTTGTGCACTCTTGATAT	2650
Db	2667	AAATGATCATTTGTCACCTGATTTTCCAACTGCAACAACTTTTGTGCACTCTTGATAT	2726
Qy	2651	AGGTATTTTTCATCGGTTGATCATGCACACCAACCAATTTTTCATTCAGTATGAACCTTG	2710
Db	2727	AGGTATTTTTCATCGGTTGATCATGCACACCAACCAATTTTTCATTCAGTATGAACCTTG	2785
Qy	2711	AGGCTGCTGCAATTTTCCACTTAACCAACCAAGCTGAAGTGAACCTTCGAAACTTGT	2770
Db	2787	AGGCTGCTGCAATTTTCCACTTAACCAACCAAGCTGAAGTGAACCTTCGAAACTTGT	2846
Qy	2771	TCATAAATCTTTTCAAAAGTTGTTTATACATCAATGTTTAAATTTTCAAAATGCTGCAGGTA	2830
Db	2847	TCATAAATCTTTTCAAAAGTTGTTTATACATCAATGTTTAAATTTTCAAAATGCTGCAGGTA	2906
Qy	2831	ATTTAATGATAAATAATTAAGTAAAGAAAGTATGTTTGCATCTTACATAGATAGATC	2890
Db	2907	ATTTAATGATAAATAATTAAGTAAAGAAAGTATGTTTGCATCTTACATAGATAGATC	2966
Qy	2891	ACAACATACAAATTCATTCAGTGCATGCTTTTATAGTGTGTTAAGCATGAGATGTACATGT	2950
Db	2967	ACAACATACAAATTCATTCAGTGCATGCTTTTATAGTGTGTTAAGCATGAGATGTACATGT	3026
Qy	2951	TACTGTTAGTCTTGCATCTGTTGCTAGTGTGATGATGAGAAAGATGTCAGGACTGGA	3010
Db	3027	TACTGTTAGTCTTGCATCTGTTGCTAGTGTGATGATGAGAAAGATGTCAGGACTGGA	3086
Qy	3011	CGTATTTTGTGCTAAAAAAGGCTGTTTGTAGGCGTTTAAATATGCTTATTTTG	3070
Db	3087	CGTATTTTGTGCTAAAAAAGGCTGTTTGTAGGCGTTTAAATATGCTTATTTTG	3146
Qy	3071	TGCTGCTCTCACTACCTATTACACACTGTTGCTTTTGGGTTTGTGTTGATGCTGCTGT	3130
Db	3147	TGCTGCTCTCACTACCTATTACACACTGTTGCTTTTGGGTTTGTGTTGATGCTGCTGT	3206
Qy	3131	GTTATACAGTAGTTTAAATTTCCATGCGAGAAAAATAAATGCTCTGAATTTCTCAAA	3184
Db	3207	GTTATACAGTAGTTTAAATTTCCATGCGAGAAAAATAAATGCTCTGAATTTCTCAAA	3260
RESULT 6			
US-10-357-930-29632			
; Sequence 29632, Application US/10357930			
; Publication No. US20040259086A1			
; GENERAL INFORMATION:			
; APPLICANT: Schlegel, Robert			
; APPLICANT: Endege, Wilson			
; APPLICANT: Monahan, John			
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR			
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF			
; TITLE OF INVENTION: HUMAN PROSTATE CANCER			
; FILE REFERENCE: MRI-007BCN			
; CURRENT APPLICATION NUMBER: US/10/357,930			
; CURRENT FILING DATE: 2003-02-04			
; PRIOR APPLICATION NUMBER: 09/785,276			
; PRIOR FILING DATE: 2003-02-16			
; PRIOR APPLICATION NUMBER: 60/183,319			
; PRIOR FILING DATE: 2000-02-17			
; PRIOR APPLICATION NUMBER: 60/189,862			
; PRIOR FILING DATE: 2000-03-16			
; PRIOR APPLICATION NUMBER: 60/207,454			
; PRIOR FILING DATE: 2000-05-25			
; PRIOR APPLICATION NUMBER: 60/211,314			
; PRIOR FILING DATE: 2000-06-09			
; PRIOR APPLICATION NUMBER: 60/219,007			
; PRIOR FILING DATE: 2000-07-18			
; PRIOR APPLICATION NUMBER: 60/255,281			
; PRIOR FILING DATE: 2000-12-13			
; NUMBER OF SEQ ID NOS: 62232			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 29632			
; LENGTH: 3499			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; LOCATION: 3490..3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499			
; OTHER INFORMATION: n = A,T,C or G			
US-10-357-930-29632			
Query Match 98.7%; Score 3164.4; DB 20; Length 3499;			
Best Local Similarity 99.8%; Pred. No. 0;			
Matches 3168; Conservative 0; Mismatches 6; Indels 0; Gaps 0;			
Qy	11	GCCTCCGGGCGAGCAGGACGGGCGGCGGCTCTGCGCGGCTCTGCGGCTCTC	70
Db	87	GAGCGCTGGCGAGGACGCGGCGGCGGCTCTGCGCGGCTCTGCGGCTCTC	146
Qy	71	GGCGGGGCGGCGGCGGCGGCTCTGCGGCTCTGCGGCTCTGCGGCTCTC	130
Db	147	GGCGGGGCGGCGGCGGCGGCTCTGCGGCTCTGCGGCTCTGCGGCTCTC	206
Qy	131	ATAAATCCATCAGAAATGACACCTTCTCAGGTTGCTTTGAAATGAAGGAACTCTTTTAC	190
Db	207	ATAAATCCATCAGAAATGACACCTTCTCAGGTTGCTTTGAAATGAAGGAACTCTTTTAC	266
Qy	191	CAGGAGAAATTTTTCGATATGTGGAAGCTGTGATGCTTTGGGAACTGGAACTCTCAAA	250
Db	267	CAGGAGAAATTTTTCGATATGTGGAAGCTGTGATGCTTTGGGAACTGGAACTCTCAAA	326
Qy	251	ATGCTGTGCTCTTCTTCCAGAGATGACACAGGTGAAGCATGCTATGGAAGCAACCA	310
Db	327	ATGCTGTGCTCTTCTTCCAGAGATGACACAGGTGAAGCATGCTATGGAAGCAACCA	386
Qy	311	TTGTAAGTCAAGTGAAGGAGTATCAGTTCAGTATCGCTACTTCAAGGGTACTTTTTAGAAC	370

QY	1352	ACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAAGGATCGGAAAG	1411
DB			
DB	667	ACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAAGGATCGGAAAG	726
QY	1412	AATCTGTGGTTTCAGGAGGAAAATTCCTTTTTCAGAAAATCAGCCATTTCCCTTCTCTTAAAGA	1471
DB			
DB	727	AATCTGTGGTTTCAGGAGGAAAATTCCTTTTTCAGAAAATCAGCCATTTCCCTTCTCTTAAAGA	786
QY	1472	TGTTTTAGAGTCTTTCCCGAAGAGATGTAGGGTTTAACTTTGAAAATAAAAATGGATCTGCC	1531
DB			
DB	787	TGTTTTAGAGTCTTTCCCGAAGAGATGTAGGGTTTAACTTTGAAAATAAAAATGGATCTGCC	846
QY	1532	AGCAAAAGGATGGATCTGGGATGGTTAACTTATCAACATATTTTGGACATGAATCTGTTTT	1591
DB			
DB	847	AGCAAAAGGATGGGATGTGGGATGGTTAACTTATCAACATATTTTGGACATGAATCTGTTTT	906
QY	1592	TGGATATAATTTTAAAAAAGCTGTTTTAGAAAATTCCTGGGAAAGAGAGAAATAGTGTGTTCTTT	1651
DB			
DB	907	TGGATATAATTTTAAAAAAGCTGTTTTAGAAAATTCCTGGGAAAGAGAGAAATAGTGTGTTCTTT	966
QY	1652	CATTTGATGAGATATTTTGCACAAATGTTTCGGGAAAAGCAGAAACAAATATCCGATACTAT	1711
DB			
DB	967	CATTTGATGAGATATTTTGCACAAATGTTTCGGGAAAAGCAGAAACAAATATCCGATACTAT	1026
QY	1712	TTTTTAAGCTCAAGGAAAATCTGAGATTTTATCCTGAACTCATGGACCTCAGATCTCGGACAA	1771
DB			
DB	1027	TTTTTAAGCTCAAGGAAAATCTGAGATTTTATCCTGAACTCATGGACCTCAGATCTCGGACAA	1086
QY	1772	CCCCATTTGCAATGAGCTTTTGACAGTTTGAAAATCTACTGGGATATAATGTACATACTG	1831
DB			
DB	1087	CCCCATTTGCAATGAGCTTTTGACAGTTTGAAAATCTACTGGGATATAATGTACATACTG	1146
QY	1832	AAGACTTGCTCAGAAAACCCATCTTATATCAAGAGCGAAAAGCTTAAGGGACTAGTCAATAT	1891
DB			
DB	1147	AAGACTTGCTCAGAAAACCCATCTTATATCAAGAGCGAAAAGCTTAAGGGACTAGTCAATAT	1206
QY	1892	TCCTGCTGGGCTGATGATACCAATGATCCTGAAACAGAGGAAATTAAGAGGAACTTGGAG	1951
DB			
DB	1207	TCCTGCTGGGCTGATGATACCAATGATCCTGAAACAGAGGAAATTAAGAGGAACTTGGAG	1266
QY	1952	TTAATGCTCTAAATTTATGATAGGATATGATTTGGATGGCTTGAAACCAACAAATATATTC	2011
DB			
DB	1267	TTAATGCTCTAAATTTATGATAGGATATGATTTGGATGGCTTGAAACCAACAAATATATTC	1326
QY	2012	AAGTGGAGCAATTTGGAAACGCTGAGCAGGAAATTTGCAGAGCTTTAAGAGCTGTTGTGTC	2071
DB			
DB	1327	AAGTGGAGCAATTTGGAAACGCTGAGCAGGAAATTTGCAGAGCTTTAAGAGCTGTTGTGTC	1386
QY	2072	CCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCCATGTGGAGT	2131
DB			
DB	1387	CCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCCATGTGGAGT	1446
QY	2132	CCAAACGCAATTTGATAACGTTGGGATATCTAGTTTTTATTTGCACAGAGGTCATTTGGGG	2191
DB			
DB	1447	CCAAACGCAATTTGATAACGTTGGGATATCTAGTTTTTATTTGCACAGAGGTCATTTGGGG	1506
QY	2192	GGGTGCAACCGCTGTTCTGGGATATCTATTTTTTCATCTAGAGCAATGTTGTGATCTATGCTTT	2251
DB			
DB	1507	GGGTGCAACCGCTGTTCTGGGATATCTATTTTTTCATCTAGAGCAATGTTGTGATCTATGCTTT	1566
QY	2252	TTGGGCTTCTCAGTTCAATGAGCAATAATGAAGTATTTAACTCTTTTCACTACAGTTCTTT	2311
DB			
DB	1567	TTGGGCTTCTCAGTTCAATGAGCAATAATGAAGTATTTAACTCTTTTCACTACAGTTCTTT	1626
QY	2312	GCAAGTATGCTATTTAAATTTACTTTGGCCAGGTATAATTTGCCAGTCACTCTTTTATAGTG	2371
DB			
DB	1627	GCAAGTATGCTATTTAAATTTACTTTGGCCAGGTATAATTTGCCAGTCACTCTTTTATAGTG	1686
QY	2372	AGAAAATTTATGCTTTAGTAAATATAAATATTTTAACTAAATATAAATCTATAATGTT	2431
DB			
DB	1687	AGAAAATTTATGCTTTAGTAAATATAAATATTTTAACTAAATATAAATCTATAATGTT	1746

RESULT 8

RESOL 8
US-10-772-636-25

US-10-772-636-23
: Sequence 25. Application US/10772636

; Sequence 23, Application 03/10/2005
; Publication No. US20050042687A1

; GENERAL INFORMATION:

; APPLICANT: Kelly, Louise M.

APPLICANT: Carroll, Joseph M.

APPLICANT: Farlow, Deborah

APPLICANT: Healy, Aileen

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,

; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,

	TITLE OF INVENTION:	9465,	23544,	7366,	27417,	57259,	21844,	943,	2061,	5891,
; TITLE OF INVENTION:	9465,	23544,	7366,	27417,	57259,	21844,	943,	2061,	5891,	

9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,	
TITLE OF INVENTION:	

; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR

; TITLE OF INVENTION: 5014

; FILE REFERENCE: MPI03-01SP1RNOMNIM

; CURRENT APPLICATION NUMBER: US/10/772,636

; CURRENT FILING DATE: 2004-02-05

; PRIOR APPLICATION NUMBER: US 60/445,241

;; PRIOR FILING DATE: 2003-02-05
;; PRIOR APPLICATION NUMBER: US 60/448,389
;; PRIOR FILING DATE: 2003-02-18
;; PRIOR APPLICATION NUMBER: US 60/456,320
;; PRIOR FILING DATE: 2003-03-20
;; PRIOR APPLICATION NUMBER: US 60/460,279
;; PRIOR FILING DATE: 2003-04-03
;; PRIOR APPLICATION NUMBER: US 60/465,924
;; PRIOR FILING DATE: 2003-04-28
;; PRIOR APPLICATION NUMBER: US 60/470,052
;; PRIOR FILING DATE: 2003-05-13
;; PRIOR APPLICATION NUMBER: US 60/498,106
;; PRIOR FILING DATE: 2003-08-26
;; PRIOR APPLICATION NUMBER: US 60/500,179
;; PRIOR FILING DATE: 2003-09-04
;; PRIOR APPLICATION NUMBER: US 60/502,909
;; PRIOR FILING DATE: 2003-09-15
;; PRIOR APPLICATION NUMBER: US 60/510,351
;; PRIOR FILING DATE: 2003-10-10
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 80
;; SOFTWARE: PaetSeq for Windows Version 4.0
;; SEQ ID NO 25
;; LENGTH: 2019
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)...(2019)
US-10-772-636-25

Query Match 63.0%; Score 2019; DB 21; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2019; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ATGACACCTTCTCAGGTGCTTGAATAGAGAACTCTTTTACAGGAGAGTCTTTT 204
DB 1 ATGACACCTTCTCAGGTGCTTGAATAGAGAACTCTTTTACAGGAGAGTCTTTT 60
QY 205 GCGATATGGAAGCTGATGCTTTGGGAACTCGAATCCTCAAAATGCTGTGGCTCTT 264
DB 61 GCGATATGGAAGCTGATGCTTTGGGAACTCGAATCCTCAAAATGCTGTGGCTCTT 120
QY 265 CTTCCAGAGATGACACAGGTGAAGCTGATGCTTATGGAAGCAACATTGTACTCAGTAGA 324
DB 121 CTTCCAGAGATGACACAGGTGAAGCTGATGCTTATGGAAGCAACATTGTACTCAGTAGA 180
QY 325 GGAGTATCAGTTCAGTATCGCTACTTCAAGGGTACTTTTGAACCAAGACTATCGGT 384
DB 181 GGAGTATCAGTTCAGTATCGCTACTTCAAGGGTACTTTTGAACCAAGACTATCGGT 240
QY 385 GGTCCATGTCAAGTGATGATGCTCAAGTGGGAGACTCATCTCAACCCAGATCAATAACC 444
DB 241 GGTCCATGTCAAGTGATGATGCTCAAGTGGGAGACTCATCTCAACCCAGATCAATAACC 300
QY 445 CTTTGAAGCGAAATTTATTATGACGATGACAAATTTGGAATCCACAATGGTGTGAA 504
DB 301 CTTTGAAGCGAAATTTATTATGACGATGACAAATTTGGAATCCACAATGGTGTGAA 360
QY 505 ACTCTGGATTCTGGATGGCTGACATGTCAGACTGGAATTAAGATTAGTTGCAATTTCT 564
DB 361 ACTCTGGATTCTGGATGGCTGACATGTCAGACTGGAATTAAGATTAGTTGCAATTTCT 420
QY 565 GAAAAACCTCTGTGTCATTAACCAAGAAAAATTAAGAAAAATCTAGATTAGGGTGAAG 624
DB 421 GAAAAACCTCTGTGTCATTAACCAAGAAAAATTAAGAAAAATCTAGATTAGGGTGAAG 480
QY 625 CTGACACTAGAGCCCTGGAGGAGATGACGATGATAGGATCTCTCCACTGTACTCCAC 684
DB 481 CTGACACTAGAGCCCTGGAGGAGATGACGATGATAGGATCTCTCCACTGTACTCCAC 540
QY 685 AAAATGTCCAATAGCTTGGAGATATCCTTTAATAGCGCAATGAGTTCAAGTCAGGCAT 744

DB 541 AAAATGTCCAATAGCTTGGAGATATCCTTTAATAAGCGCAATGAGTTCAAGTCAGGCAT 600
QY 745 TCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAG 804
DB 601 TCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAG 660
QY 805 ACGATGGAACACAGATAAACCTGGAACATACTTTGATTTTTTCGAAGAAGATCTCAGTGAG 864
DB 661 ACGATGGAACACAGATAAACCTGGAACATACTTTGATTTTTTCGAAGAAGATCTCAGTGAG 720
QY 865 CACGTAGTTACGGGTGATGCCCTTCTCGACATGTGGGTACAGCTTGCTCTTATCATCC 924
DB 721 CACGTAGTTACGGGTGATGCCCTTCTCGACATGTGGGTACAGCTTGCTCTTATCATCC 780
QY 925 ACCATTGCTGAGAGTGAAGAGTCTCGAATTTCTTACTCTTCCCATCATGAGCAGAAAT 984
DB 781 ACCATTGCTGAGAGTGAAGAGTCTCGAATTTCTTACTCTTCCCATCATGAGCAGAAAT 840
QY 985 TCCCGGAAAAAATAGGCAAGTGAAGTGTGATATATAATTTAAGCCATTACAGGA 1044
DB 841 TCCCGGAAAAAATAGGCAAGTGAAGTGTGATATATAATTTAAGCCATTACAGGA 900
QY 1045 TACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATTGGAAGCCCAAGATACCATTTGAT 1104
DB 901 TACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATTGGAAGCCCAAGATACCATTTGAT 960
QY 1105 GTTGGCCATCGAGGTGCGAGAACTCTACAACTGCCCAGCTGCTAAAGTTCAAGAA 1164
DB 961 GTTGGCCATCGAGGTGCGAGAACTCTACAACTGCCCAGCTGCTAAAGTTCAAGAA 1020
QY 1165 AATACTATTGCTTCTTTAAGAAATGCTGTAGTCAATGCTGAGCCCTTTGTAGAAATTGAC 1224
DB 1021 AATACTATTGCTTCTTTAAGAAATGCTGTAGTCAATGCTGAGCCCTTTGTAGAAATTGAC 1080
QY 1225 GTAACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGACT 1284
DB 1081 GTAACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGACT 1140
QY 1285 ATGAAAAGAAATTTGATGCTGATCCAGTTCAGTTGAATTTTGAATTCAGTAAAGAAATTA 1344
DB 1141 ATGAAAAGAAATTTGATGCTGATCCAGTTCAGTTGAATTTTGAATTCAGTAAAGAAATTA 1200
QY 1345 ACATTTGACCAACTCCAGTGTGTTAAAGCTCACATGTCAGTGCATGCACTGAAATCTAAGGAT 1404
DB 1201 ACATTTGACCAACTCCAGTGTGTTAAAGCTCACATGTCAGTGCATGCACTGAAATCTAAGGAT 1260
QY 1405 CGGAAAGAAATCTGTGTTTCAAGGAGAAATTCCTTTTTCAGAAATCAGCCATTTCTTCT 1464
DB 1261 CGGAAAGAAATCTGTGTTTCAAGGAGAAATTCCTTTTTCAGAAATCAGCCATTTCTTCT 1320
QY 1465 CTTAAGATGTTTATAGTCTTTTCCAGAGAGATGTAGGGTTTAAACATTGAAATTAAGTGG 1524
DB 1321 CTTAAGATGTTTATAGTCTTTTCCAGAGAGATGTAGGGTTTAAACATTGAAATTAAGTGG 1380
QY 1525 ATCTGCCAGCAAGGGATGGAATGTGGGATGTAACCTTATCAACATATTTTGAATGATG 1584
DB 1381 ATCTGCCAGCAAGGGATGGAATGTGGGATGTAACCTTATCAACATATTTTGAATGATG 1440
QY 1585 CTGTTTTTGGATATAATTTTAAAACTGTTTTTGAATAATCTGGAAGAGAGAGATGAGT 1644
DB 1441 CTGTTTTTGGATATAATTTTAAAACTGTTTTTGAATAATCTGGAAGAGAGAGATGAGT 1500
QY 1645 TTTTCTTCAATTTGATGAGATATTTTGCACAAATGTTTCCGCAAGAGAGAGAGATATCCG 1704
DB 1501 TTTTCTTCAATTTGATGAGATATTTTGCACAAATGTTTCCGCAAGAGAGAGAGATATCCG 1560
QY 1705 ATACTATTTTAACTCAAGGAAATCTGAGATTTTATCTGAACCTCATGGACCTCAGATCT 1764
DB 1561 ATACTATTTTAACTCAAGGAAATCTGAGATTTTATCTGAACCTCATGGACCTCAGATCT 1620
QY 1765 CGGACAAACCCCATTTGCAATGAGCTTTGCAAGTTTGAATAATCTACTGGGGATTAATGTA 1824
DB 1621 CGGACAAACCCCATTTGCAATGAGCTTTGCAAGTTTGAATAATCTACTGGGGATTAATGTA 1680

Db 988 CGCTGGATCCTTACTCTTCCCATCATGACGAGAAGTTCAGAAAAAATATAGGCAAG 1047
Qy 1007 TGAGATTGACTATATATTAATTAAGCATATACAGGATACAGTTGGACATGAATCTT 1066
Db 1048 TCAGATTGATTTTATCATCATCAAGCCATTAACCCAGGATATAGTTGTTCTATGACGCTT 1107
Qy 1067 CATTTTCAAGTATTTGGAGCAAGATACCATTTGGATTTGGCCATCGAGGTGCAGAA 1126
Db 1108 CATTTTCAAGTATTTGGAAACCAAGATACCACTGGATTTGGACATCGTGGTGCAGGA 1167
Qy 1127 ACTCTACAACACTGCCAGCTGGCTAAAGTTCAAGAAAAATATATTTGCTTTTAAAGAA 1186
Db 1168 ACTCAACAACTGCCAAGCTGGCTAAAGTACAGGAATATATTTGCTTTTAAAGAA 1227
Qy 1187 ATGCTGCTAGTCACTGTCAGCCTTTTGPAGATTTGACGTACACCTTTCAAGGACTTTG 1246
Db 1228 ATGCTGCCAGCAGTGGTGCAGCAATTTTGGAAATTTGATGTCACCTTTCAAGGACTTAG 1287
Qy 1247 TGCCCGTGGTATATCATGATCTTACCTGTTGTTGACTATCAAAAAGAAATTTGATGCTG 1306
Db 1288 TGCCGTGTAGTATCATGATCTCACCTGCTGTTAACTATGAAAAGGAAATATGAAGCTG 1347
Qy 1307 ATCCAGTTGAATTTTGAATTTCCAGTAAAGAAATTAACATTTGACCAACTCCAGTTGT 1366
Db 1348 ATCCAGTTGAATTTTGAATTTCCAGTAAAGAAATTAACATTTGACCAACTCCAGTTAT 1407
Qy 1367 TAAAGCTCACTCATGCTGACCTGCACTGAAATTAAGGATCGGAAGAAATCTGTGTTGAG 1426
Db 1408 TGAAGCTTCTCATGCTGACTGCACTAAAAACCAAGACCAAGAAACATGTATGCTGAGG 1467
Qy 1427 AGGAAATTCCTTTTCAAGAAATCAGCAATTTCCCTTCTTTAAGATGTTTTAGAGCTT 1486
Db 1468 AGGAAATTCCTTTTCAAGAAATTCCTTCTTTAAGATGTTTTAGAGCTAT 1527
Qy 1487 TGCCAGAGATGAGTTTACATTTGAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1546
Db 1528 TGCCAGAAATGAGATTTATATAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAA 1587
Qy 1547 TGTGGATGCTTAATCTATCAACATATTTTGAATGAATCTGTTTTTGGATATAATTTTAA 1606
Db 1588 TATGGACCGCACTTATCGACATATTTTGAATGAATGCAATTTTGGATATAATTTTAA 1647
Qy 1607 AAATCTTTTGAATAATCTGGAGAGAGAGATAGTTTCTTCTCATTTGATGACAGATA 1666
Db 1648 AAATCTTTTGAATAATCTGGAGAGAGAGATAGTTTCTTCTCATTTGATGACAGATA 1707
Qy 1667 TTTGCAATGTTTGGCAAGACGACAAATATCCGATCTATTTTAACTCAAGAA 1726
Db 1708 TCTGTACATGTTTGGCAAGACGACAAATATCCGATCTATTTTAACTCAAGAA 1767
Qy 1727 AATCTGAGATTTTATCTGAACTCATGACCTCAGATCTCGGACAAACCCCATTTGCAATGA 1786
Db 1768 AGTCTGACATTTTACCTGAACTCATGACCTCAGATCTCGGACAAACCCCATTTGCAATGA 1827
Qy 1787 GCTTTGCACAGTTTGAATAATCTACTGGGATAAATGTAATATGAGAACTTGTCTCAGAA 1846
Db 1828 GCTTTGCACAGTTTGAATAATTTTGGGATAAATGCCATATCTGAAGATCTCTTAGAA 1887
Qy 1847 ACCATCTTATTTCAAGGCAAAAGCTTAAGGACTAGTCAATTTCTCTGGGGTATG 1906
Db 1888 ACCATCTTATTTCAAGGCAAAAGCTTAAGGACTAGTCAATTTCTCTGGGGTATG 1947
Qy 1907 ATACCAATGATCTGAAACAGAGAAATTTGAAGAACTTGGAGTTAATGTTCTAATTT 1966
Db 1948 ATACCAATGATCTGAAACAGAGAAATTTGAAGAACTTGGAGTTAATGTTCTAATAT 2007
Qy 1967 ATGATAGG 1974
Db 2008 ATGATAGG 2015

; Sequence 48, Application US/10426776
; Publication NO. US20040009553A1
; GENERAL INFORMATION:
; APPLICANT: Gluckman, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsia, Fong-Ying
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Kapeller-Ibermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 88, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; TITLE OF INVENTION: 86604 AND 32222 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0620NMIM
; CURRENT APPLICATION NUMBER: US/10/426,776
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229,662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795,691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105,992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406,045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314,881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161,188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-426-776-48

Query Match 30.9%; Score 991; DB 17; Length 2393;
Best Local Similarity 80.1%; Pred. No. 1.1e-217;
Matches 1418; Conservative 0; Mismatches 265; Indels 88; Gaps 18;

Qy 1284 TATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGAATTTCCAGTAAAGAAATTTCCCTTC 1343
Db 61 TTTCTAATAGAAATATGAAGCTGATCCAGTTGAAATTTGAAATTTCCAGTAAAGAAATTTCCCTTC 120
Qy 1344 AACATTTGACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACCTGCACTGAAATCTAAGGA 1403
Db 121 AACATTTGACCAACTCCAGTTTATGAAGCTTCTCATGTGACCTGCACTGAAATCTAAGGA 180
Qy 1404 TCGGAAAGAAATCTGTGGTTTCAGGAGGAAATTTCCCTTTTCAGAAATCAGCCATTTCCCTTC 1463
Db 181 CCAGAAACATATGATGCTGAGGAGGAAATTTCCCTTTTCAGAAACCAACCAATTTCCCTTC 240
Qy 1464 TCTTAAGATGTTTTAGAGTCTTTTCCAGAGAGATGTAGGGTTTTAACTTGAATAAATAATG 1523
Db 241 TCTTAAGATGTTTTAGAGTCAITGGCCAGAAATTTAGGATTTTATATAGAAATTAATG 300
Qy 1524 GATCTGCCAGCAAAAGGGATGGAATGTGGGATGTAATCTTCAACATATTTTGCATGAA 1583


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; ORGANISM: Homo sapiens
US-09-796-692-4214

Query Match      16.3%; Score 522.4; DB 9; Length 524;
Best Local Similarity 99.8%; Pred. No. 6.1e-110;
Matches 523; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2405 AAACCTAAATATATAAATCTAATGTTAAACATATGTTCAATTAAGCATAGCATTGGA 2464
Db 1 AAACCTAAATATATAAATCTAATGTTAAACATATGTTCAATTAAGCATAGCATTGGA 60

QY 2465 AATTAACCTATATAAATAGCTCATATTTACACTTACAGCTTTTCAATTTGATCAGTCTGAA 2524
Db 61 AATTAACCTATATAAATAGCTCATATTTACACTTACAGCTTTTCAATTTGATCAGTCTGAA 120

QY 2525 ATCTTTAGCCTTAAAGGAAATGACTATGCTAATATTAACCTGACCAATGAAAAAATAAG 2584
Db 121 ATCTTTAGCCTTAAAGGAAATGACTATGCTAATATTAACCTGACCAATGAAAAAATAAG 180

QY 2585 TACCTCAAAATGATGCTATTTGACCTGCTGATGCTCAATGCAAAATCTTTGTGCTATCTT 2644
Db 181 TACCTCAAAATGATGCTATTTGACCTGCTGATGCTCAATGCAAAATCTTTGTGCTATCTT 240

QY 2645 GTATATAGTATTTTACATGGGTTGACATGCGACACAAACCACTTTTCAATTCAGTATGA 2704
Db 241 GTATATAGTATTTTACATGGGTTGACATGCGACACAAACCACTTTTCAATTCAGTATGA 300

QY 2705 ACCTTGAGGCTGCTGCCATTTTCCACTTTAAACCAACAGGCTGAAAGGTGAACCTCGAAA 2764
Db 301 ACCTTGAGGCTGCTGCCATTTTCCACTTTAAACCAACAGGCTGAAAGGTGAACCTCGAAA 360

QY 2765 CTTGTTTCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGC 2824
Db 361 CTTGTTTCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGC 420

QY 2825 AGGTAATTTAATGATATAAATATTAGTAAGAAAAAGTATGTTATGCTACTTAGTAGAA 2884
Db 421 AGGTAATTTAATGATATAAATATTAGTAAGAAAAAGTATGTTATGCTACTTAGTAGAA 480

QY 2885 TAGATCACAACATACAAATTCATTCAGTGCATGCTTTAGGTGT 2928
Db 481 TAGATCACAACATACAAATTCATTCAGTGCATGCTTTAGGTGT 524

RESULT 12
US-10-040-862-4214
; Sequence 4214, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
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; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4214
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-4214

Query Match      16.3%; Score 522.4; DB 14; Length 524;
Best Local Similarity 99.8%; Pred. No. 6.1e-110;
Matches 523; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2405 AAACCTAAATATATAAATCTAATGTTAAACATATGTTCAATTAAGCATAGCATTGGA 2464
Db 1 AAACCTAAATATATAAATCTAATGTTAAACATATGTTCAATTAAGCATAGCATTGGA 60

QY 2465 AATTAACCTATATAAATAGCTCATATTTACACTTACAGCTTTTCAATTTGATCAGTCTGAA 2524
Db 61 AATTAACCTATATAAATAGCTCATATTTACACTTACAGCTTTTCAATTTGATCAGTCTGAA 120

QY 2525 ATCTTTAGCCTTAAAGGAAATGACTATGCTAATATTAACCTGACCAATGAAAAAATAAG 2584
Db 121 ATCTTTAGCCTTAAAGGAAATGACTATGCTAATATTAACCTGACCAATGAAAAAATAAG 180

QY 2585 TACCTCAAAATGATGCTATTTGACCTGCTGATGCTCAATGCAAAATCTTTGTGCTATCTT 2644
Db 181 TACCTCAAAATGATGCTATTTGACCTGCTGATGCTCAATGCAAAATCTTTGTGCTATCTT 240

QY 2645 GTATATAGTATTTTACATGGGTTGACATGCGACACAAACCACTTTTCAATTCAGTATGA 2704
Db 241 GTATATAGTATTTTACATGGGTTGACATGCGACACAAACCACTTTTCAATTCAGTATGA 300

QY 2705 ACCTTGAGGCTGCTGCCATTTTCCACTTTAAACCAACAGGCTGAAAGGTGAACCTCGAAA 2764
Db 301 ACCTTGAGGCTGCTGCCATTTTCCACTTTAAACCAACAGGCTGAAAGGTGAACCTCGAAA 360

QY 2765 CTTGTTTCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGC 2824
Db 361 CTTGTTTCATAAATCTTTCAAAAGTTGTTTACATCAATGTTAAATTTCAAAATGCTGC 420

QY 2825 AGGTAATTTAATGATATAAATATTAGTAAGAAAAAGTATGTTATGCTACTTAGTAGAA 2884
Db 421 AGGTAATTTAATGATATAAATATTAGTAAGAAAAAGTATGTTATGCTACTTAGTAGAA 480

QY 2885 TAGATCACAACATACAAATTCATTCAGTGCATGCTTTAGGTGT 2928
Db 481 TAGATCACAACATACAAATTCATTCAGTGCATGCTTTAGGTGT 524

RESULT 13
US-10-057-475B-4214
; Sequence 4214, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
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Db	301	ACCTTGAGGCTGCTGCCAATTTTCCACTTACCAACACGAGCTGAAGGTGACCTCGAA	360
Qy	2765	CTTGTGTTTCAATAATCTTTTCAAAAGTGTGTTTACATCAATGTTTAAATTTCAAAATGCTGC	2824
Db	361	CTTGTGTTCAATAATCTTTCAAAAGTGTGTTTACATCAATGTTTAAATTTCAAAATGCTGC	420
Qy	2825	AGGCTAATTTAATGTTATATAATTTAGTAGAGAAAAAGTATGTTATTCATACACTTAGTAGAA	2884
Db	421	AGGCTAATTTAATGTTATATAATTTAGTAGAGAAAAAGTATGTTATTCATACACTTAGTAGAA	480
Qy	2885	TAGATCAACATACATAAAATTTCAATTCAGTCATGCTTTAGGTGT	2928
Db	481	TAGATCAACATACATAAAATTTCAATTCAGTCATGCTTTAGGTGT	524

RESULT 15

US-10-764-324-4214

; Sequence 4214, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10467

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4214

; LENGTH: 524

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-764-324-4214

Query Match	16.3%;	Score 522.4;	DB 19;	Length 524;
Best Local Similarity	99.8%;	Pred. No. 6.1e-110;		
Matches 523;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;

Qy	2405	AAACTAAATATATAATCTATATGTTAAACATATGTTCAATTAAGCATAGCAGCACTTTGA	2464
Db	1	AAACTAAATATATAATCTATATGTTAAACATATGTTCAATTAAGCATAGCAGCACTTTGA	60
Qy	2465	AAATTAACATATAAAATAGTCATATTTACATTCAGCTTTTCATTGATCAGGTCCTGAA	2524
Db	61	AAATTAACATATAAAATAGTCATATTTACATTCAGCTTTTCATTGATCAGGTCCTGAA	120
Qy	2525	ATCTTTAGCACTTAAGGAAAAAGCATGTCATGCAATAATTATACCTGACCAATGAAAAAATAAG	2584

Db	121	ATCTTTAGCACCTTAAGGAAAAATGACTATGCATAAATTATACCTGACCATGAAAAAATAAG	180
Qy	2585	TACCTCAAAATGCATGATTTGCACCTGGTGATTCCAAATGACCAAAATCTTTGTGCCATCTT	2644
Db	181	TACCTCAAAATGCATGATTTGCACCTGGTGATTCCAAATGACCAAAATCTTTGTGCCATCTT	240
Qy	2645	GTATATAGGTATTTTTTACATGGGTTGACATGCACACAACACCATTTTCAATCAGTATGA	2704
Db	241	GTATATAGGTATTTTTTACATGGGTTGACATGCACACAACACCATTTTCAATCAGTATGA	300
Qy	2705	ACCTTGAGGCTGCTGCCATTTTTTCCACTTAAACCAACCAGCCTGAAGGTGAACCTCGAAA	2764
Db	301	ACCTTGAGGCTGCTGCCATTTTTTCCACTTAAACCAACCAGCCTGAAGGTGAACCTCGAAA	360
Qy	2765	CTTGTGTTTCATAAATCTTTCAAAAAGTGTGTTTACATCAATGTTAAAAATTTCAAATGCTGC	2824
Db	361	CTTGTGTTTCATAAATCTTTCAAAAAGTGTGTTTACATCAATGTTAAAAATTTCAAATGCTGC	420
Qy	2825	AGGGTAATTTAAATGTATAAAAATTTAGTAGAAAAAAGTATGTATTGCATCTTTAGTAGAA	2884
Db	421	AGGGTAATTTAAATGTATAAAAATTTAGTAGAAAAAAGTATGTATTGCATCTTTAGTAGAA	480
Qy	2885	TAGATCACACATACAAAATTCAAATTCAGTGCATGCTTTTAGGTGT	2928
Db	481	TAGATCACACATACAAAATTCAAATTCAGTGCATGCTTTTAGGTGT	524

Search completed: July 3, 2005, 00:06:53
Job time : 1867 secs

Search completed: July 3, 2005, 00:06:53
Job time : 1867 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 06:48:25 ; Search time 5762 Seconds

(without alignments)
4439.290 Million cell updates/sec

Title: US-10-047-855-3

Perfect score: 3537

Sequence: 1 MTPQVAFIRGTLPGVEF.....LCGSDIHVDANGINDVNA 672

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n_model -DEV=xlh
-Q=/cgm2_1/USPTO_spool/US10047855/runat_01072005_155529_2232/app_query.fasta_1.839
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10047855@cgm 1.1 4352 @runat_01072005_155529_2232 -NCPU=6 -ICPU=3
-NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gssi:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3331.5	94.2	3142	3 AK030645	Mus muscu
2	3318.5	93.8	3614	3 AK050318	Mus muscu
3	3150	89.1	3248	3 BC006887	Mus muscu
4	3066	86.7	3578	3 AK031658	Mus muscu
5	2400	67.9	2604	3 AK009563	Mus muscu
6	2143	60.6	1618	3 AK049491	Mus muscu
7	2119	59.9	2228	3 AK051728	Mus muscu
8	1570	44.4	1006	5 BX344123	BX344123
9	1486.5	42.0	1128	4 BM478430	BM478430 AGENCOURT

10	1365.5	38.6	901	6 CB196769	CB196769 AGENCOURT
11	1322	37.4	882	4 BM457674	BM457674 AGENCOURT
12	1321	37.3	818	5 BX403389	BX403389
13	1319.5	37.3	783	6 CD466056	CD466056 Leukon2 1
14	1305	36.9	958	5 BU503488	BU503488 AGENCOURT
15	1285	36.3	948	5 BU145581	BU145581 AGENCOURT
16	1260	35.6	754	7 CN303372	CN303372 170006000
17	1248	35.3	833	4 B1144681	B1144681 602909978
18	1227.5	34.7	855	6 BQ962080	BQ962080 AGENCOURT
19	1223.5	34.6	805	6 CA317224	CA317224 UI-M-FW0-
20	1218.5	34.5	878	5 BQ930039	BQ930039 AGENCOURT
21	1216.5	34.4	728	7 CN303370	CN303370 170004243
22	1216	34.4	696	2 AW327746	AW327746 dr01904.x
23	1186	33.5	688	4 BM786845	BM786845 K-EST0065
24	1185	33.5	711	5 BX507382	BX507382 DKE2p779K
25	1156.5	32.7	691	7 CK833283	CK833283 4057562 B
26	1153.5	32.6	821	4 B1822275	B1822275 603036411
27	1148.5	32.5	836	5 BU519577	BU519577 AGENCOURT
28	1135	32.1	770	6 CB236281	CB236281 AGENCOURT
29	1132	32.0	786	7 CO795305	CO795305 AGENCOURT
30	1104	31.2	719	7 CO433958	CO433958 UI-M-HX0-
31	1103	31.2	660	6 BY709247	BY709247 BY709247
32	1102.5	31.2	768	1 AU136888	AU136888 AU136888
33	1095.5	31.0	795	4 BG623187	BG623187 602648092
34	1089	30.8	667	7 CK832619	CK832619 4056677 B
35	1075	30.4	665	6 BY734861	BY734861 BY734861
36	1066.5	30.2	760	7 CF286044	CF286044 AGENCOURT
37	1056	29.9	748	7 CO559324	CO559324 AGENCOURT
38	1041	29.4	667	6 CD771503	CD771503 AGENCOURT
39	1032.5	29.2	665	6 CD640091	CD640091 AGENCOURT
40	1030	29.1	764	7 CV073042	CV073042 AGENCOURT
41	1015.5	28.7	621	7 CK623779	CK623779 mil3e07.y
42	1007	28.5	642	2 BB652394	BB652394 BB652394
43	994.5	28.1	746	7 CN303375	CN303375 170005318
44	994	28.1	578	7 CV024277	CV024277 1525 Full
45	986	27.9	861	7 CO554090	CO554090 AGENCOURT

ALIGNMENTS

RESULT 1	AK030645	3142 bp	linear	HTC 03-APR-2004
AK030645	Mus musculus	6 days neonate head cDNA, RIKEN full-length enriched library, clone:5430401018 product:hypothetical Glycero-phosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.		
LOCUS	AK030645	3142 bp	mRNA	
DEFINITION	AK030645.1	GI:26326638		
ACCESSION	AK030645	HTC; CAP trapper.		
VERSION	AK030645.1	Mus musculus (house mouse)		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS	High-efficiency full-length cDNA cloning			
TITLE	Meth. Enzymol. 303, 19-44 (1999)			
JOURNAL	99279253			
MEDLINE	10349636			
PUBMED	10349636			
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
TITLE	Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL	20499374			
MEDLINE	11042159			
PUBMED	11042159			
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 3142)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. .3142
/organism="Mus musculus"
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/db_xref="FANTOM,DB:5430401018"
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/db_xref="GI:26326639"
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polyA_signal /note="putative"
3142
polyA_site /note="putative"
ORIGIN
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Pred. No.: 0 Matches: 624
Score: 3331.50
Percent Similarity: 97.04%
Conservative: 31
Best Local Similarity: 92.44%
Mismatch: 17
Query Match: 94.19%
Indels: 3
DB: 3 Gaps: 1
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QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrLeuValLeuSerArg 60
Db 277 ATTAATGAAACAGAGAGGAGACAGTGTCTGCGAAAGCAGTGTCTCTCAATAGA 336
QY 61 GlyValSerValGlnTrpArgTrpPheLysGlyTyPheLeuGluProLysThrIleGly 80
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Db 1957 CTGAAGGAATTTGGAGTAAATGGTCTAATATATATAGGATATATGATGGATCCCTGAA 2016
Qy 618 GlnProAsnIlePheGlnValGlnGluLeuArgLeuLysGlnGluLeuProGluLeu 637
Db 2017 CAGCAATATATTTCCAAGTTGGAGCAGTTGGAGCGCTGAAGCAAGAAATTTGCCAGAGCTT 2076
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RESULT 2
LOCUS AK050318 3614 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone: C730037B04 product: hypothetical Glycero-phosphoryl diester phosphodiesterase/Glycosyl hydrolase, starch-binding domain containing protein, full insert sequence.
ACCESSION AK050318
VERSION AK050318.1 GI:26093898
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
DEFINITION The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 5
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Konno, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissue was provided by William A. Held, Roswell Park Cancer Institute, Department of Molecular and Cellular Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES

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Query Match: 93.82% Indels: 4
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ACCESSION BC006887
VERSION BC006887.1 GI:14711816
KEYWORDS HTc.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 3248)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusik, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,
Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 3248)
Strausberg, R.
Direct Submission
Submitted (27-APR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgobcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louisege, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 16 Row: 1 Column: 21
This clone was selected for full length sequencing because it
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analysis
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AK031658 3578 bp mRNA linear HTC 03-APR-2004
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DEFINITION enriched library, clone:6030473012 product:hypothetical
Glycerophosphoryl diester phosphodiesterase/Glycosyl hydrolase,
starch-binding domain containing protein, full insert sequence.
ACCESSION AK031658
VERSION AK031658.1 GI:26082447
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE
JOURNAL

High-efficiency full-length cDNA cloning
Meth..Enzymol. 303, 19-44 (1999)
99279253
MEDLINE
PUBMED
10349636

REFERENCE
AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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11042159

REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
MEDLINE
PUBMED
11076861

REFERENCE
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

TITLE
JOURNAL

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3578)

REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takanashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

1. 3578

/organism="Mus musculus"

/mol_type="mRNA"

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FEATURES
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ORIGIN

Alignment Scores:
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Best Local Similarity: 86.54% Mismatches: 17
Query Match: 86.68% Indels: 46
DB: 3 Gaps: 2

US-10-047-855-3 (1-672) x AK031658 (1-3578)

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Qy 40 uLeuProGlnAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerAr 60
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Qy 60 gGlyValSerValGlnTrpArgTyrPheLysGlyTyrPheLeuGluProLysThrIleG 80
Db 385 AGGAGTGTGAGTGAAGTACCGCTACTTTCAGAGGCTGCTTTTATAGAACCAAGACTATCGG 444
Qy 80 YGlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleTh 100
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Qy 100 rProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisGlyValG 120
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Qy 120 uThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSe 140
Db 553 ----- 553
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Qy 160 sLeuThrIleuGluGlyLeuGluGlu-----AspAspAspArgValSerProTh 177
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Qy 177 rValLeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLy 197
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Db	1041	ACCATTGGAGTGGCATCGTGTGTCAGGAACTCAACAACGACTGCGCAAGCTAGCTAA	1100	LOCUS	Mus musculus adult male tongue	cDNA	RIKEN full-length enriched		
QY	337	sValGlnGluAsnThrIleAlaSerIleuArgAenAlaAaSerHisGlyAlaAlaPheVa	357	DEFINITION	library, clone:31003216 product: hypothetical glycerophosphoryl				
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QY	377	sCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProVa	397	KEYWORDS	Mus musculus (house mouse)				
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QY	397	lLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLyl	417	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Db	1281	AAAAGAAATTAACATTTGACCAACTCCAGTTATTGAAGCTTTCTCATGTGACTGCAATAA	1340	REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;				
QY	417	eSerLysAspArgLysGluSerValGlnGluGluAsnSerPheSerGluAsnGlnPr	437	AUTHORS	Carninci, P. and Hayashizaki, Y.				
Db	1341	AAACCAAGACCGGAACAACATCTTTGTATGAGGAGGAAATTTCTTTCTGAAATCAGCC	1400	TITLE	High-efficiency full-length cDNA cloning				
QY	437	oPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGl	457	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
Db	1401	ATTTCCTCTCTTAAGATGGTTTATGAATCATTTGCCAGAAATGTAGGATTTAATATAGA	1460	MEDLINE	99279253				
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QY	477	eAspMetAsnLeuPheLeuAspIleLeuLysThrValLeuGluAsnSerGlyLysAr	497	AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
Db	1521	TGATATGAATGGTTTTTGGATATAATTTTAAAAAAGCTTTTAAAGAAATTTCTGGGAAG	1580	JOURNAL	Ito, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
QY	497	gArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAs	517	MEDLINE	Normalizaton and subtraction of cap-trapper-selected cDNAs to				
Db	1581	GAGATAGTGTCTCTCTTTGATGTCAGATATTGTACAATGTTTCGGCAGAGCAGAA	1640	PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes				
QY	517	nLysTyrProIleLeuPheLeuThrGlnGlySerGluIleTyProGluLeuMetAs	537	REFERENCE	Genome Res. 10 (11), 1757-1771 (2000)				
Db	1641	CAAAATATCCATATATTTTGGACCAAGGAAGCTGATATTTTACCCCACTCAGGA	1700	AUTHORS	20530913				
QY	537	pLeuArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlu	557	TITLE	11076861				
Db	1701	CCTCAGATCTCGAACACACCTTTGCAATGAGTTTGCAGTTTGAATAATTTTGGG	1760	JOURNAL	The RIKEN Genome Exploration Research Group Phase II Team and the				
QY	557	yIleAsnValHisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAl	577	MEDLINE	FANTOM Consortium.				
Db	1761	GATAAATGCCATCTAGAGACCTCTCTTAGAAACCCATCTATGTCCAAAGAGGCAAGC	1820	PUBMED	Functional annotation of a full-length mouse cDNA collection				
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Db	1821	TAAGGATTTGGTATATCTCTGCTGGGGTGATGATACCAACCATCTCTGAAACAGAGGAA	1880	AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research				

Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, F., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayaehizaki, Y.

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

PLEASE VISIT OUR WEB SITE (<http://genome.gsc.riken.jp/>) FOR FURTHER DETAILS.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGAGATTCGAGTTAATTAATCCGCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

source

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CDS

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ORIGIN

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US-10-047-855-3 (1-672) x AK009563 (1-2604)

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Qy	431	SerPheSerGluAsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGlu	450
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US-10-047-855-3 (1-672) x AK049491 (1-1618)

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 QY 255 AlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeu 274
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 DB 1203 CGAGAGCTTAAGAACTGTTGTGCTCCACTGTGACCACTTCATCTCTCTCTCTCT 1262
 QY 655 GlyGluSerAspIleHisValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
 DB 1263 GTGGAGCCTGATATCCAGCTGATGCCAAGCGCATTTGATAGTGTGGAGAACGCT 1316

RESULT 7
 AK051728 2228 bp mRNA linear HTC 03-APR-2004
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 Glycrophosphoryl diester phosphodiesterase/Glycosyl hydrolase,
 starch-binding domain containing protein, full insert sequence.
 AK051728
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 VERSION HTCC; CAP trapper.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Mech. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636
 2
 REFERENCE
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159
 3
 REFERENCE
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 4
 REFERENCE
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE
 AUTHORS Nature 420, 563-573 (2002)
 6 (bases 1 to 2228)
 Adachi, J., Aizawa, K., Akimura, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S.,
Takeda, Y., Tanaka, T., Tonaru, A., Toyota, T., Yasunishi, A.,
Murasato, M., and Havaishizaki, Y.

TITLE
JOURNAL

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT

FAX: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.

FEATURES

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CDS

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VENA"

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ORIGIN

Alignment Scores:	5.98e-230	Length:	2328
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DB:	3		

US-10-047-855-3 (1-672) x AK051728 (1-2228)

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Qy 263 AlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArg 282

61	GCTGAGAGTGAAGAAGCGCTGGAATCCTTACTCTTCCCATCATGACGAGAAATTCAGA	120	Db
283	LysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGlyTyrSer	302	Qy
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303	CysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAspValGly	322	Qy
181	IGTCTTATGCAGTCTTCATTTCCAAGTATTGGAAACCAAGAAATACCATTCGACGTTGGA	240	Db
323	HisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsnThr	342	Qy
241	CATCGTGGTCAGGGAACCTCAACACAGACTGCCAAGCTAGCTAAAGTACAGAAAAATCT	300	Db
343	IleAlaSerLeuArgAsnAlaAlaSerHisSGlyAlaAlaPheValGluPheAspValHis	362	Qy
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363	LeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMetLys	382	Qy
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383	LysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPhe	402	Qy
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403	AspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLys	422	Qy
481	GACCAACTCCAGTTATTGAAGCTTCTCATGTGACTGTGCATTAANAACCAAGACCGGAAA	540	Db
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443	MetValLeuGlnSerLeuProGlnAspValGlyPheAsnIleGluLysTrpIleCys	462	Qy
601	ATGGTTTTAGATCATTTGCCAGAAATGTAGGATTTAATATAGAATAAATATGGATTCG	660	Db
463	GlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPhe	482	Qy
661	CAACACAGGATCGAGTATGGGATGGCACTTATCAACATATTTTGATATGAATGTGTTT	720	Db
483	LeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSer	502	Qy
721	TTGGATATATTTTAAAAACTGTTTTAGAAAAATTCCTGGGAAGAGGAGAATAGTGTTCCT	780	Db
503	SerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeu	522	Qy
781	TCCTTTTGATCAGATATTTGTACAATGGTTTCGGCAGAACGACGAAACAATATCCCATTTA	840	Db
523	PheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThr	542	Qy
841	TTTTTTGACCCAGGAAAGTCTGATATTACCCCGAACTCATGACCTCAGATCTCGACA	900	Db
543	ThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThr	562	Qy
901	ACACCAATGCAATGAGTTTTGCACAGTTTGAATAATTTTGGGGATAAATGCCCATCT	960	Db
563	GluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIle	582	Qy
961	GAAACCTCTCTTAGAAACCCATCCTATGTCTCCAGAGGCAAAAGCTAAGGATTTGGTCATA	1020	Db
583	PheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGly	602	Qy
1021	TTCTGCTGGGGTGATGATACCAACGATCTTGAAACAGAGGAAACTGAAGGAATTTGGA	1080	Db
603	ValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnIlePhe	622	Qy
1081	GTAATGGTCTTAATATATGATAGGATATATGATTGGATGCTGACAGCCAAATATATTC	1140	Db
623	GlnValGluGlnLeuLeuArgLeuLysGlnGluLeuProGluLeuLysSerCysLeuCys	642	Qy
1141	CAAGTGGAGCAGTTGGAGCGCTCGAAGCAGAAATTCGACAGCTTAAGACTGTTTGTGT	1200	Db

QY 643 ProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHisValAsp 662
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RESULT 8
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 LOCUS BX344123 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1059YA01 5-PRIME, mRNA sequence.

ACCESSION BX344123
 VERSION BX344123
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1006)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT On May 1, 2003 this sequence version replaced gi:30311247.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9838.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CS1A10152E01Q1&c=9838.r.

FEATURES

source

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 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
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ORIGIN

Alignment Scores:
 Pred. No.: 8,33e-168 Length: 1006
 Score: 1570.00 Matches: 311
 Percent Similarity: 97.50% Conservative: 1
 Best Local Similarity: 97.19% Mismatches: 3
 Query Match: 44.39% Indels: 8
 DB: 5 Gaps: 0

US-10-047-855-3 (1-672) x BX344123 (1-1006)

QY 344 AlaSerLeuArgAsnAlaAalaSerHisGlyAlaAlaPheValGluPheAspValHisLeu 363
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QY 364 SerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLys 383
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 Db 91 TCAAGAGCACTTGTGCGCGGTATATCATCATCTTACCTGTTGTTGACTATGAAAAAG 150

QY 384 LysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAsp 403
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QY 404 GlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGlu 423
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 Db 211 CAACCTCCAGTTGTTAAAGCTCACTCATGTGACTGCMCTGAAATCTAAGGATCGGAAGAA 270

QY 424 SerValValGlnGlnGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMet 443
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 Db 271 TCTGTGGTTTCAGAGGAAAAATTCCTTTTCAGAAAAATCAGCCATTTCTCTTCTTAAGATG 330

QY 444 ValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTyrIleCysGln 463
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QY 464 GlnArgAspGlyMetTrrPaspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeu 483
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QY 504 PheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPhe 523
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RESULT 9
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 LOCUS AGENCOURT 6508010 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5578502
 DEFINITION 5', mRNA sequence.

ACCESSION BM478430
 VERSION BM478430.1 GI:18527472
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1128)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12333 row: k column: 15
High quality sequence stop: 618.
Location/Qualifiers
1. 1128
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dn.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

FEATURES
source

ORIGIN

Alignment Scores:
Pred. No.: 3 47e-158 Length: 1128
Score: 1486.50 Matches: 324
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US-10-047-855-3 (1-672) x BM478430 (1-1128)

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DB 603 AAATCTAAGGATCGAAAGAATCTGTGTTTCAGAGGAAATTCCTTTTCAGAAATCAG 662
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QY 552 PheGluAsnLeu---LeuGlyIleAsnValHisThr--GluAspLeuLeuArgAsn-Pro 569
DB 1023 TTTGAAAAATTCACCTGGGGGATTAAGTACCTACTCTGAGAACTTGCTCAAAACCCCT 1082
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DB 1083 TCCCAATTTCAAAGCAAAAGTCTAAGGA 1112

RESULT 10

LOCUS CB196769
DEFINITION AGENCOURT 11258308 NIH MGC 135 Mus musculus cDNA clone
IMAGE:30135584 5', mRNA sequence.

ACCESSION CB196769
VERSION CB196769.1 GI:28224876

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 901)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-f@mail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM0033 row: n column: 09

High quality sequence stop: 660.

FEATURES
source

1. 901 Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_135"

/note="vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI;
Normalized full-length enriched library from pooled mouse
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14.5, and 15.5 (size selected for the 0.5-1 kb fragments)
Cloned directionally, priming method: Oligo-dT. cDNA
enrichment: >1k bp. Average insert size 1.6k bp.
Normalization (cot value): 7.5 kb. Priming sequence:
5'-GACTAGTCTAGATCGGCGCGCC(C)3'. Tissue contributed
by, David Rowe. Library constructed by ResGen, Invitrogen
Corp.

ORIGIN

Alignment Scores:

Pred. No.: 1-59e-144 Length: 901
Score: 1365.50 Matches: 276
Percent Similarity: 95.6% Conservatives: 11
Best Local Similarity: 92.00% Mismatches: 5
Query Match: 38.61% Indels: 9
DB: 6 Gaps: 1

US-10-047-855-3 (1-672) x CB196769 (1-901)

QY 102 LeuGluSerGluIleIleAspGlyGlnPheGlyIleHisAsnGlyValGluThr 121
DB 12 CTAGAAAGTGAATCATTTATTCAGCATGACAGTTTGGCATCCACAATGGTGTGAACA 71
QY 122 LeuAspSerGlyTyrLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGlu 141
DB 72 CTGGATTCTGGATGCTTACATGTGAGCTGAATAAGATTGCGTCTGCATTTTCTGAG 131
QY 142 LysProValSerIleThrLysLysLysLeuLysSerArgPheArgValLysLeu 161
DB 132 AAACCTCTGTTTCAATTAGCAAGAAAAGTTCAAAAATCGAGATTAGGTGAAGCTC 191
QY 162 ThrLeuGluGlyLeuGluGlu-----AspAspAspAspArgValSerProThrVal 178
DB 192 ACACCTCGAGGCTCTGGAGGAAGATGATGATGATGATGATGATGATGATGATGATG 251
QY 179 LeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCys 198
DB 252 CTTTCAAAATGTCACACAGCCTGGAGATATCTTAAATGAAGTGAATGAGTTCAGTGC 311
QY 199 ArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTyrThrGluTyrSer 218
DB 312 AGGCACTACAGCCAGATGGGTATGGCTTACAGCCGATCGTTGACAGAGTACAGC 371
QY 219 IleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeu 238
DB 372 ATACAGACAATGGAACCAAGATAATCTGGAGCTCATCTTTGACTTTTGGAGGAATCTC 431
QY 239 SerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeu 258
DB 432 AGTGAGCATGTAGTTTCAGGGTGTATGTTCTCTGGACACGTTGGCACAGCATGCTCCTG 491
QY 259 SerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer 278
DB 492 TCTTCTACATGCTGAGAGTGGGAAGCGCTGGAATCTTACTCTTCCCATCATGAGC 551
QY 279 ArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeu 298
DB 552 AGAAATCCAGAAAACATATAGGCAAGTCAGAGTTGATTTATCATCATCAAGCCATTA 611
QY 299 ProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTyrPheProArgIlePro 318
DB 612 CCTGATATAGTGTGTCTATGTCAGTCTTCAATTTTCCAAAGTATTTGAAACCAAGATACCA 671
QY 319 LeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGluLeuAlaLysVal 338
DB 672 TTGGACGTTGGACATCGTGGTGGCANGGAACCTCAACAGCATGCCAGCTAGCTAAGTA 731
QY 339 GlnGluAsnThrIleAlaSerLeuArgAsnAlaLaSerHisGlyValAlaPheValGlu 358
DB 732 CAGGAAATACTATCGCTTCTTTAA- AATGCTGCCAGTCTATGGCGCAGCATTTGTAGAA 790
QY 359 PheAspValHisLeu-SerLysAsp-PheValProValValTyrHisAsp-LeuThrCys 377

DB 791 TTTGATGTCACCTTTTCAAAGGACTTTTGTGCGCGGTGTATCATGAACTCACCTGC 850
QY 378 CysLeuThrMetLysLysLysPheAsp-AlaAspProVal-GluLeuPhe 393
DB 851 TGTCTGACCATGAAGGAATATGAAGCTGTATCCCGTTTGAATTTGTTT 900

RESULT 11

BM457674

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

EMAIL

TISSUE

CDNA

LIBRARY

ARRANGED

BY

AGENCY

CLONE

DISTRIBUTION

INFORMATION

CAN

BE

FOUND

THROUGH

THE

I.M.A.G.E.

CONSORTIUM

LLNL

AT

HTTP://

IMAGE.LBL.NOV

PLATE

L1AM12131

ROW

D

COLUMN

07

HIGH

QUALITY

SEQUENCE

STOP

652

FEATURES

LOCATION

QUALIFIERS

1..882

/organism

=Homo sapiens"

/mol_type

=mRNA"

/db_xref

=taxon:9606"

/clones

=IMAGE:5498838"

/tissue_type

=lymphoma, cell line"

/lab_host

=DH10B (phage-resistant)"

/clone_lib

=NIH_MGC_85"

/note

=Organ: lymph; Vector: pCMV-SPORT6; Site: 1: NotI;

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.867 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1-43e-139 Length: 882
Score: 1322.00 Matches: 251
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 37.38% Indels: 0
DB: 4 Gaps: 0

US-10-047-855-3 (1-672) x BM457674 (1-882)

QY 422 LysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSerLeu 441
DB 1 AAAGAATCTGTGGTTCAGGAGGAAAATTCCTTTTCAGAAAATCAGCCATTTCTCTCT 60
QY 442 LysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTyrPhe 461
DB 61 AAGATGTTTGTAGAGTCTTTGCCAGAGAGATGTAGGGTTTAAACATTTGAAATAAATGGATC 120
QY 462 CysGlnGlnArgAspGlyMetTyrAspGlyAsnLeuSerThrTyrPheAspMetAsnLeu 481
DB 121 TGCAGCAAGGAGTGAATGTGGATGGTAACCTTATCAACATATTTGACATGAATCTG 180
QY 482 PheLeuAspIleLeuLeuLysThrValLeuGluAsnSerGlyLysArgIleValPhe 501

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Db 181 TTTTGGATATAATTTTAAACTGTTTTAGAAAAATTCGGGAAGAGAGAGATAGTGT 240
Qy 502 SerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIle 521
Db 241 TCTTCATTGATGCAGATATTGTCACAAATGGTTCCGCAAAAGCAGACAAATATCCGATA 300
Qy 522 LeuPheLeuThrGlnGlyLeuSerGluIleTyrProGluLeuMetAspLeuArgSerArg 541
Db 301 CTATTTTAACTCAAGGAAATCTGAGATTTATCCTGAATCTATGGACCTCAGATCTCGG 360
Qy 542 ThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHis 561
Db 361 ACAACCCCATTCGATGAGCTTTGCACAGTTTGAAATCTACTGGGGATAAATGATCAT 420
Qy 562 ThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuVal 581
Db 421 ACTGAAGACTTGCTCAGAAACCCATCTATATTCAGAGGCAAAAGCTAAGGGAGTAGTC 480
Qy 582 IlePheCysTyrGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeu 601
Db 481 ATATTCTGCTGGGGTGATGATACCAATGATCCTGAAACACAGAGAAATTTGAAGGAACCT 540
Qy 602 GlyValLeuGlnLeuIleTyrAspArgIleTyrAspTyrMetProGluGlnProAsnIle 621
Db 541 GGAGTTAATAGTCTTAATTTATGATAGGATATATGATGGATGCTGACCAACCAATATA 600
Qy 622 PheGlnValGluGlnLeuGluArgLysGlnGlnLeuProGluLeuLysSerCysLeu 641
Db 601 TTCCAAGTGGAGCAATTCGAACGCTGAAGCAGGAATTCGCAGAGCTTAAGAGCTGTGTTG 660
Qy 642 CysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHisVal 661
Db 661 TGTCCCACTGTGTAGCGCTGTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCATGTG 720
Qy 662 AspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 721 GATGCCAAGCGCAATGATAACGTGGAGATGCT 753

RESULT 12
BX403389 818 bp mRNA linear EST 28-APR-2004
LOCUS BX403389 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1059YA01 5-PRIME, mRNA sequence.
ACCESSION BX403389
VERSION BX403389.2 GI:46846825
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 818)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001).
On May 13, 2003 this sequence version replaced gi:30615152.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and EcoRV
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9838.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS5AA0152D05RMI&c=9838.r.
Location/Qualifiers
1. .818
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1059YA01"
FEATURES
source

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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/Note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

```

Alignment Scores: 1.64e-139 Length: 818
Pred. No.: 1321.00 Matches: 261
Score: 96.35% Conservative: 3
Percent Similarity: 96.35% Mismatches: 7
Best Local Similarity: 95.26% Indels: 3
Query Match: 37.35% Gaps: 0
DB: 5
US-10-047-855-3 (1-672) x BX403389 (1-818)
Qy 345 SerLeuArgAsnAlaAspSerHisGlyAlaLapheValGluPheAspValHisLeuSer 364
Db 3 TCTTTAAGAAATGCTGCTAGTCATGTCAGCCTTTGTAGAAATTTGACGTACACCTTTCA 62
Qy 365 LysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLys 384
Db 63 AAGGACTTTGTGCCGTGGTATATCATGATCTTACCTGTGTGCTATGAAAAAGAAA 122
Qy 385 PheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGln 404
Db 123 TTTGATGCTGATCCAGTTGAAATTTATTTGAAATTTCCAGTAAAGAAATTAACATTTGACCAA 182
Qy 405 LeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSer 424
Db 183 CTCAGTTGTTAAAGCTCACTCATGTGACTGCACATGAAATCTAAGGATCGGAAAGAACTCT 242
Qy 425 ValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetVal 444
Db 243 GTGGTTTCAGGAGGAAATTCCTTTTCAGAAAAATTCAGCCATTTTCCTTCTCTTAAGATGGTT 302
Qy 445 LeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTyrIleCysGlnGln 464
Db 303 TTAGAGTCTTTGCGAAGATGATGAGGTTTAACTTGAATTAATAATGGATCTGCCAGCAA 362
Qy 465 ArgAspGlyMetTyrAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAsp 484
Db 363 AGGATGGATGCGGATGGTAACTTATCAACATATTTTGACATGAATCTGTTTTGGAT 422
Qy 485 IleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPhe 504
Db 423 ATAATTTTAAAAACTGTTTAGAAAAATTCCTGGGAAGAGGAGATAGTGTTCCTTCATTT 482
Qy 505 AspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeu 524
Db 483 GATGCAGATATTTGCACAAATGGTTCGGCAAAAGCAGAAACAATATCCGATCTATTTTAA 542
Qy 525 ThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrPro 544
Db 543 ACTCAAGAAAAATCTGAGATTTATCTGAATCTATGACCTCAGACCTCAGATCTGGCAACCC 602
Qy 545 IleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAsp 564
Db 603 ATTGCAATGAGCTTTGCACAGTTTTGAAATCTACTGGGGATAAATGTACATACCTGAAAC 662
Qy 565 LeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCys 584
Db 663 TTGCTCAGAAACCCATCTATATTCAGAAAGGCAAAAGCTAAGGAGCTAGTCATATCTGCG 722
Qy 585 TrrGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAs 604
Db 723 TGGGGTGATGATCCCAATGATTCCTGAAACAGAGAGAAATTTGAGGAACTTGGAGTTAA 782
Qy 604 n-GlyLeuIleTyrAspArgIleTyrAsp-TripMet 615
Db 783 TGGGCCTAAATTTTGGATAGGAAATATGATTTGGATG 818

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RESULT 13

CD466056 783 bp mRNA linear EST 04-JUN-2003
 LeukN2_1_G06_g1_A024 Unstimulated peripheral blood leukocytes N2
 Equus caballus cDNA clone LeukN2_1_G06_A024 5', mRNA sequence.

ACCESSION

CD466056

VERSION

CD466056.1 GI:31387324

KEYWORDS

EST.

SOURCE

Equus caballus (horse)

ORGANISM

Equus caballus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

REFERENCE

1 (bases 1 to 783)

AUTHORS

Vandenplas, M., Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S.,
 Moore, J. N., Liang, C., Sun, F., Sullivan, R., Shah, M. and Pratt, L. H.

TITLE

An EST database from equine (Equus caballus) unstimulated

JOURNAL

peripheral blood leukocytes

COMMENT

Unpublished (2003)

Other ESTs: LeukN2_1_G06_b1_A024

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 593 0210

Email: mmpratt@uga.edu

Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in

the Human Genome Center, University of Tokyo Institute of Medical

Science; tissue and RNA were prepared in the Department of Large

Animal Medicine, University of Georgia; sequencing done in the

Laboratory for Genomics and Bioinformatics, University of Georgia.

Sequence ends have been trimmed to exclude vector and regions below

phred quality 16. Three-prime sequences are presented as their

reverse complement and have been trimmed to exclude polyA.

Seq primer: Sugs (CTCTGCTCTAAAGCTGCG).

Location/Qualifiers

1..783

/organism="Equus caballus"

/mol_type="mRNA"

/strain="thoroughbred"

/db_xref="taxon:9796"

/clone="LeukN2_1_G06_A024"

/sex="male"

/tissue type="blood"

/cell type="leukocytes"

/lab_host="DH108-T1 phage-resistant E. coli"

/clone_lib="unstimulated peripheral blood leukocytes N2"

/note="Organ: circulatory system; Vector: pME18S-FL3;

Site 1: XhoI; Site 2: XhoI; The library was prepared from

polyA+ RNA from unstimulated equine peripheral blood

leukocytes isolated from a healthy adult horse.

Double-stranded cDNA was cloned unidirectionally into

different DraIII sites of the pME18S-FL3 vector (5-prime

DraIII site is CACTGTGTG, 3-prime DraIII site is

CACCATGTG). XhoI excises the cDNA insert."

ORIGIN

Alignment Scores:

Pred. No.: 2,276-139 Length: 783

Score: 1319.50 Matches: 257

Percent Similarity: 98.85% Conservativity: 1

Best Local Similarity: 98.47% Mismatches: 2

Query Match: 37.31% Indels: 2

DB: 6 Gaps: 1

US-10-047-855-3 (1-672) x CD466056 (1-783)

QY 158 ArgValLysLeuThrLeuGluGlyLeuGluAspAspArgValSerProThr 177

DB 3 ACGGTAAAGTCACTAGAGGTCTGGAGGAGAGTACGATGAGGTCTCCACT 62

QY 178 ValLeuHisLysMetSerAsnSerLeuGluLeuSerLeuLeuSerAspAsnGluPhelys 197

Db 63 GTTCTTCAAAAATGTCAACAGCCTGGAGATATCGTTAATAAGTCAACATGAGTTCAAG 122

QY 198 CysArgHisSerGlnProGluCysGlyTyrglyLeuGlnProAspArgTrrThrGluTyr 217

Db 123 TGCAGGCATTACAGCCGGAGTGGGTATGGCTTACAGCTGATCGCTGACGGAGTAT 182

QY 218 SerTleGlnThrMetGluProAspAsnLeuGluLeuPheAspPheGluGluasp 237

Db 183 AGCATACAGACAATGGAACCGGATAAAGCTGGAATGATATTCGATTTTGTGA---GAT 238

QY 238 LeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeu 257

Db 239 CTCAGTGAACATATGATTCAGGGCGATGCCCTTCCTGGACATGGGGTACAGCGTGCCTC 298

QY 258 LeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMet 277

Db 299 TTATCATCCACCATGTCTGAGAGTGGGAGAGTCTGGATCTTACTCTTCCCACATCATG 358

QY 278 SerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleLeuLysPro 297

Db 359 AGCAGAAATTCAGGAAACAAATAGGCAAGTGAAGTGTACTATATAATTTAAGCCA 418

QY 298 LeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTrrPheProArgIle 317

Db 419 TTACCAGGATACAGTTGTGCATGAAATCTTCATTTTCCAAAGTACTGGAAGCCAAGATA 478

QY 318 ProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLys 337

Db 479 CCATTGAGTGTGGGCATCGAGGTGCAGGAAATCTACACAACTGCTCAGCTTGCTAAA 538

QY 338 ValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheVal 357

Db 539 GTTCAAGAAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGCTGCGACGCTTTGTA 598

QY 358 GluPheAspValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCys 377

Db 599 GAATTTGATGTACATCTTTCAAAAGATTTTGTGCTGGTGTATCATGATCTCACCTGT 658

QY 378 CysLeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProVal 397

Db 659 TGTTTGACTATGAAGAAATTTGATGCTGATCGATTGATTTGAATTTCCAGTA 718

QY 398 LysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLys 417

Db 719 AAGGAATTAACATTTGACCAGCTCCAGTTGTTAAAGCTGCTCATGCTGACTGCACCTAAA 778

QY 418 Ser 418

Db 779 TCT 781

RESULT 14

BU503488

LOCUS

AGENCOURT 8968328 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491134

DEFINITION

5', mRNA sequence.

ACCESSION

BU503488

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 958)

AUTHORS

NIH-MGC http://mgs.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

linear EST 12-SEP-2002

BU503488 958 bp mRNA

AGENCOURT 8968328 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6491134

DEFINITION

5', mRNA sequence.

ACCESSION

BU503488

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 958)

AUTHORS

NIH-MGC http://mgs.nci.nih.gov/

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM14042 row: a column: 23
High quality sequence stop: 597.

FEATURES

Location/Qualifiers
1..958
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clones="IMAGE:6491134"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dr primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.44e-137 Length: 958
Score: 1305.00 Matches: 266
Percent Similarity: 89.44% Conservative: 22
Best Local Similarity: 82.61% Mismatches: 19
Query Match: 36.90% Indels: 17
DB: 5 Gaps: 4

US-10-047-855-3 (1-672) x BU503488 (1-958)

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QY 169 AspAspAspArgValSerProThr-ValLeuHisLysMetSerAsnSerLeuGluIl 188
DB 1 CATGATGACGATAAGGTCTCTCCACTGGTCTTCCACAAAATGTCACACGCTGGAGAT 60
QY 188 eSerLeulleSerAspAsnGluPheLysCysArgHisSerGlnProGluCysGlyTyrGl 208
DB 61 ATCCTTAATAGTGAACAATAGTTCAGGTGACGAGGCACTCAGCCAGAAATGTGGGTATGG 120
QY 208 YLeuGlnProAspArgTyrThrGluTyrSerIleGlnThrMetGluProAspAsnLeuGl 228
DB 121 CTTACAGCCCGATCGTTGGACAGAGTACAGCATACAGACATGGAACCATATCTGGA 180
QY 228 uLeullePheAspPheGluGluAspLeuSerGluHisValValGlnGlyAspAlaLe 248
DB 181 GCTCATCTTTGACTTTTGTAGGAAGATCTCAGTCAGCATGTAGTTCAGGGTGATGTTCT 240
QY 248 uProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSe 268
DB 241 TCGTGACACGCTGGGCACAGCATGCTCTGCTCTTACCATGTCTGAGGTGGAGGAAG 300
QY 268 rAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysThrIleGlyLysVa 288
DB 301 CGCTGGAATCCTTACTCTTCCCATCATGACGAGAAATTCAGAAAAATATAGGCAGAA 360
QY 288 lArgValAspTyrIleIleLysProLeuProGlyTyrSerCysAspMetLysSerSe 308
DB 361 CAGAGTTGATTTATCATCATCAAGCAATACCTGGATATAGTTCCTTATGACGTCTTC 420
QY 308 rPheSerLysTyrTyrPheProArgIleProLeuAspValGlyHisArgGlyValaGlyAs 328
DB 421 ATTTTCCAAGTATTTGAAACCAAGATACCATTTGGACGCTTGGACATCGGTGGCAGGGAA 480
QY 328 nSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAs 348
DB 481 CTCACACAGCAGTCGCCAGTAGCTAGTAAGTACAGGAAATATATTCGCTCTTTTAAAGAA 540
QY 348 nAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheVa 368
DB 541 TGTGCGCAGTCATGGCGCAGCATTTGTAGAAATTTGATGTCACCTTTCAAGGACTTTGT 600
QY 368 lProValValTyrHisAspLeuThrCysCysLeuThrMetLysLeuLysPheAspAlaAs 388
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Alignment Scores:

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DB 601 GCCCGTGTGTATCATGACCTCACCTGTCTGTGACCATGAGAGGAATATGAAGCTGA 660
QY 388 pProValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLe 408
DB 661 TCCAGTTGAATGTTTGAATCCCAAGTAATACCAATTTGACCAATCCAGTATT 720
QY 408 uLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGl 428
DB 721 GAAGCTTTCTCATGTGACTGG-CTTAAAAAACCAAGACCGGGAACATCTTTGTATGAGA 779
QY 428 uGluAsn-SerPheSerGluAsnGlnProPheProSer-LeuLysMetValLeuGluSer 447
DB 780 GGAAAAATTTTCTTCTGAAAAATCAGCCATTTCTCTCTAAAGAGGGTTTAAAGAAATC 839
QY 448 LeuProGlu---AspValGlyPheAsn---IleGluIleLysTyrIleCysGlnGlnArg 465
DB 840 ATTTCCAGAAAAATGTAGGATTTTCTAATTGAATTACAAATGGA-ATTGCCCCACCC 898
QY 466 AspGly-----MetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPhe 482
DB 899 CAGGGAATGGAATAATAATATGGATGGC-----CCCAACTTATTTC 937
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RESULT 15

BU145581 948 bp mRNA linear EST 03-SEP-2002
LOCUS AGENCOURT 8125917 Lupski dorsal root ganglion Homo sapiens cDNA
DEFINITION Clone IMAGE:6177333 5', mRNA sequence.

ACCESSION

BU145581

VERSION

BU145581.1 GI:22659113

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 948)

AUTHORS

NIH-MGC <http://imgc.ncbi.nih.gov/>.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabps-f@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM13555 row: b column: 22

High quality sequence stop: 653.

FEATURES

Location/Qualifiers

1..948

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6177333"

/sex="male"

/tissue_type="dorsal root ganglia"

/dev_stage="adult, 36 yr"

/lab_host="DH10B"

/clone_lib="Lupski dorsal root ganglion"

/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:

NotI; Site_2: SalI; cDNA made by oligo-dr priming.

Directionally cloned using the following adaptors:

5'-TCGACCCACGCGCCG-3' and

5'-GACTAGTTCGTAGTCGCGAGCGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

Pred. No.: 2,72e-135 Length: 948
Score: 1285.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.33% Indels: 0
DB: 5 Gaps: 0

US-10-047-855-3 (1-672) x BUI45581 (1-948)

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Db 63 GAAGATGTAGGGTTTAAACATTGAATAAAATGGATCTGCCAGCAAAAGGATGGAATGTGG 122
Qy 470 AspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAspIleIleLeuLysThr 489
Db 123 GATGGTAACCTTATCAACATATTTTGACATGAATCTGTTTTTGGATATATATTTTAAAAACT 182
Qy 490 ValLeuGluAsnSerGlyLysArgIleValPheSerSerPheAspAlaAspIleCys 509
Db 183 GTTTTAGAAAATCTGGGAGAGGAGATAGTGTCTTCTCATTTGATGCAGATATTTGCC 242
Qy 510 ThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrGlnGlyLysSer 529
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Qy 610 ArgIleTyrAspTyrMetProGluGlnProAsnIlePheGlnValGluGlnLeuGluArg 629
Db 543 AGGATATATGATTGGATGCTGACCAACCAATATATTTCCAAAGTGGAGCAATTTGGAACGC 602
Qy 630 LeuLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSerArgPheVal 649
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Qy 650 ProSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIleAspAsnVal 669
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Qy 670 GluAsnAla 672
Db 723 GAGAATGCT 731
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Job time : 5796 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 07:07:40 ; Search time 929 Seconds
(without alignments)
3248.529 Million cell updates/sec

Title: US-10-047-855-3

Perfect score: 3537

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 13051180 seqs, 2245448946 residues

Total number of hits satisfying chosen parameters: 26102360

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MAIRIX=blasmus62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1399	39.6	2393	12	US-11-136-527-4018 Sequence 4018, Ap
3	1005	28.4	2792	12	US-11-097-143-5114 Sequence 5114, Ap

Sequence 5113, Ap	12	5439	26.1	922	US-11-097-143-5113
Sequence 27182, A	12	2392	18.9	667	US-11-097-143-27182
Sequence 26897, A	12	2457	18.9	667	US-11-097-143-26897
Sequence 26896, A	7	7162	18.9	667	US-11-097-143-26896
Sequence 27181, A	8	9667	18.9	667	US-11-097-143-27181
Sequence 19967, A	9	2299	18.8	666	US-11-097-143-19967
Sequence 19866, A	10	4299	18.8	666	US-11-097-143-19866
Sequence 40595, A	11	661	18.7	661	US-11-097-143-40595
Sequence 40594, A	12	4220	18.7	661	US-11-097-143-40594
Sequence 1279, Ap	13	634.5	17.9	693	PCT-US05-00517-1279
Sequence 33686, A	14	550	15.5	2100	US-11-097-143-33686
Sequence 33685, A	15	550	15.5	4100	US-11-097-143-33685
Sequence 2598, Ap	16	434	14.0	3657	US-10-932-182A-2598
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Sequence 10470, A	28	195	5.3	4001	US-60-655-875-10470
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Sequence 1469, Ap	36	174	4.9	2089378	US-10-526-324-1469
Sequence 1838, Ap	37	174	4.9	2089378	US-10-526-324-1838
Sequence 1355, Ap	38	174	4.9	2089378	PCT-1803-06509-1355
Sequence 34240, A	39	172.5	4.8	605	US-10-703-032-34240
Sequence 88995, A	40	169.5	4.5	636	US-60-655-875-88995
Sequence 96527, A	41	159.5	4.5	481	US-60-655-875-96527
Sequence 74699, A	42	150	4.2	2615	US-60-655-875-74699
Sequence 11318, A	43	148.5	4.2	2848	US-60-655-875-11318
Sequence 1012, Ap	44	148.5	4.2	2848	US-11-031-175-1012
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ALIGNMENTS

RESULT 1

US-11-136-527-4005

; Sequence 4005, Application US/11136527

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; CURRENT FILING DATE: 2005-05-25

; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4005

; LENGTH: 3381

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-4005

Alignment Scores:

Pred. No.:	1.04e-263	Length:	3381
Score:	2965.50	Matches:	571
Percent Similarity:	90.76%	Conservative:	38
Best Local Similarity:	85.10%	Mismatches:	33
Query Match:	83.84%	Indels:	29
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21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40	1260 TTTGATGTCCACTTTCAGAGACTTAGTGCCTGTAGTATCATGATCTCACCTGCTGT 1319
246 GCAATGTGTGAAACTGTGATGCCTTGGGAACTGGAGTCTCAAAATGCTGTGCCT--- 302	379 LeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluLeuProValLys 398
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101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120	1500 CCTTCTCTTAAGATGGTTTAGAGTCATTGCCAGAAAATGTAGGATTTAATATAGAATA 1559
480 CCTTTAGAAAACGAAATCATATTACCATGGACAAATTTGGAATCCAAATGGTGTGAA 539	459 LysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAsp 478
121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140	1560 AAATGGATTTGCCAACACACAGGATGGAGTATGGCGCGCAACTTATCGACATATTTTGAT 1619
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141 GluLysProProValSerIleThrLysLysLeuLysLysSerArgPheArgValLys 160	1620 ATGAATGCATTTTGGATATTAATTTTAAAACTGTTTATAGAAATTCGCGGAAGAGAGA 1679
600 GAGAACTCTCTGTTTCAATTAACCAAGAAAAGTTCAAAAATCTAGATTTAGGGTAAAG 659	499 IleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLys 518
161 LeuThrLeuGluGlyLeuGlu-----AspAspAspAspArgValSerProThrVal 178	1680 ATAGTATTTCTTCAITTTGATGCAGACATCTGTACAATGGTTCGGCAGAAACAAACAAA 1739
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179 LeuHisLysMetSerAsnSerLeuGluIleSerLeuLysLeuAspAsnGluPheLysCys 198	1740 TATCCCATATATTTTGAAGCAAGGAAAGTCTGCATTTTACCCTGAACCTCATGGACCTC 1799
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279 ArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeu 298	2019 -----TGTGTTTTGTAATAAATCTCCATGGAATGTTTCAACAGTGTAGTTTATCTA 2072
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1140 CTGATGTTGGACATCTGTGTGAGGAACTCAACACAACTGCCAAGCTGGCTAAAGTA 1199	
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RESULT 2

US-11-136-527-4018
; Sequence 4018, Application US/11136527
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

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; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4018
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4018

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Score: 1399.00 Matches: 261
Percent Similarity: 95.8% Conservative: 16
Best Local Similarity: 90.31% Mismatches: 12
Query Match: 39.55% Indels: 0
DB: 12 Gaps: 0

US-10-047-855-3 (1-672) x US-11-136-527-4018 (1-2393)

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DB 371 GATATAATTTAAAACTGTTTGAAGAAATTCGGGAGAGAGAGAGATATTTCTTCA 430
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DB 731 AATGCTCTAATATATGATAGGATATACGATTCGATTCGCTGAACACCAATATATTCNA 790
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DB 939 HisLeuGlnProArgSerIleThrProLeuGluSerGluIleIleIleAspGlyGln 112
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DB 791 GTGGAGCAACTGGAGCGCTGAAGCGAGAAATTCAGAGACTTAAGAACTGTTGTGTCCC 850
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QY 664 AsnGlyIleAspAsnValGluAsnAla 672
DB 911 AACGCGATTGATAATGTGGAACGCT 937

RESULT 3
US-11-097-143-5114
; Sequence 5114, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5114
; LENGTH: 2792
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-5114

Alignment Scores:
Pred. No.: 3,4e-82 Length: 2792
Score: 1005.00 Matches: 250
Percent Similarity: 52.29% Conservative: 116
Best Local Similarity: 35.71% Mismatches: 244
Query Match: 28.41% Indels: 91
DB: 12 Gaps: 22

US-10-047-855-3 (1-672) x US-11-097-143-5114 (1-2792)

QY 14 LeuLeuProGlyGluValPheAlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsn 33
DB 529 CTGGCGCCCAACGACGAGTTCGCCATAGTGGTAAATTCGAGCGCTCGGCAACTGGCAG 588
QY 34 ProGlnAsnAlaValAlaLeuLeuPro---GluAsnAspThrGlyGluSerMetLeuTrp 52
DB 589 CACTCGGAGCGGCTATTTTGTCCAAAATGAGGAGGACAAATGAGTAGTAGTCTGTGG 648
QY 53 LysAlaThrIleValLeuSerArgGlyValSerValGlnTyrArgTyrPheLysGlyTyr 72
DB 649 ACAGGAGAGATCTATATTCCGCGTCACCTGTGCACACGGAATATCGCTATATGTC---TGT 705
QY 73 PheLeuGluProLysThrIleGlyGlyProCysGlnValIleValHisLysTrpGluThr 92
DB 706 GCCGTCGATCCC-----GGCAGGAGCAGCTGATTTGTCGCCGCTTGGGAAACG 753
QY 93 HisLeuGlnProArgSerIleThrProLeuGluSerGluIleIleIleAspGlyGln 112
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Db 754 CAATTACAGCCCCGAATAGTCAAGAGTTGGATGAGCAGCCTGCCAAGAAATCAGAGTGAC 813
Qy 113 ---PheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTyrLeuThrCysGlnThr 131
Db 814 ATATTGGCTCGTTCAATGGCCAGAGAGGTGGATCGGGCTGCTGACCAAGGAGACT 873
Qy 132 GluIleArgLeuArgLeuHisTyrSerGluLysProValSerIleThrLysLysLys 151
Db 874 CTGGTGACGCTAAAGTCTTTTATGCT-----CGTTTCAGCTTT---AAGCAGCGC 921
Qy 152 LeuLysLysSerArgPheArgValLysLeuThrLeuGluGlyLeuGlu-----GluAsp 169
Db 922 ATGAACCTAGGACATATCCAGGTCAAGTCAAGCGCCCATGAACCTGAGTATTCACAGTGCC 981
Qy 170 AspAspArgValSerProThrValLeuHisLysMetSerAsnSerLeu-----186
Db 982 GGCTGTGATACCATGCTGCCCTCG-----TCTCCATGGAGGATTCCTGTGCAACGAC 1035
Qy 187 -----GluIle 188
Db 1036 ACTCATGATACCAAGAGNACGGCGTGAATCTCCACAGCCTTTGCGCTTTAGCGAGTGC 1095
Qy 189 SerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnProGluCysGlyTyrGly 208
Db 1096 GTCACCTTGAGTGGCCAGAGTGCAGAAATCAGA---AGTCAAGAGCAGCTTCGGCACCGGC 1152
Qy 209 LeuGlnProAspArgTyrThrGluTyrSerIleGlnThrMetGluProAspAsnLeuGlu 228
Db 1153 TGTGGACCCACCGATTTGGTTATATTCATCCATCGACCGTGGAGACTTCGAGNACACGGCC 1212
Qy 229 LeuIlePheAspPheGluGluAspLeuSerGluHisValValGlnGlnAspAlaLeu 248
Db 1213 TACCTGATTGATTGTAC-----AGCTACAGCTCCCGGTGGCCCAAGAGATGGTCCA 1266
Qy 249 ProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerClyLysSer 268
Db 1267 CCGAACCACTTGGCTATCATATTATGTGTCGCCAATCTTTTAA-----CGTTCT 1317
Qy 269 AlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysThrIleGlyLysVal 288
Db 1318 GAAGGCAACTTGGATGGCCCATAACTGTGCCAAGGCCATCGACCTTCGGAATGATG 1377
Qy 289 ArgValAspTyrIleIleLysProLeuProGlyTyrSerCys-----AspMet 305
Db 1378 CGTCTGGTATCTTATCGTGAAG-----CCCTCATCGTGTGCTCTAATGGATATG 1431
Qy 306 LysSerSerPheSerLysTyrTrpLysProArg---IleProLeuAspValGlyHisArg 324
Db 1432 AGTGTACAGCTATGCCGATATCTGAAACAGCAAGTGGACGGGACTGGATGTGGGCCATCGT 1491
Qy 325 GlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAla 344
Db 1492 GGTTCGGAATACTAGT---TTCAAGGCCAAGGACGCTGTTATTCGGAGATACCATTACT 1548
Qy 345 SerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSer 364
Db 1549 TCITTTGAAGATGCCGAGACGATGTGTCGACATGTGTGAGTTTCGATGTCCAACCTAGC 1608
Qy 365 LysAspPheValProValTyrHisAspLeuThrCysCysLeuThrMetLysLysLys 384
Db 1609 AAGGATCTGGTGGCCAGTGGTATACAGATTTTCATGATCTATGTTTCACTAAAGTCCGAG 1668
Qy 385 PheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGln 404
Db 1669 TGCAGTCTGCAGGACGACGATTTCTCGCTCTACCGATGAGGAGTTGTCCTCGGAGCAG 1728
Qy 405 LeuGlnLeuLysLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSer 424
Db 1729 TTGAAGAAATTGAAGTCTATCATCTGCT-----GAGGGT 1764
Qy 425 ValValGlnGluGluAsnSerPheSer-----GluAsnGlnProPhePro 439
::: ::::
```

```
Db 1765 CTGTCAGGAGACGCGTTTCGTTTCCAAACGATGATTGTTAGACACACGCGCTTCCG 1824
Qy 440 SerLeuLysMetValLeuLeuSerLeuProGluAspValGlyPheAsnIleGluIleLys 459
Db 1825 CAGCTATCGATGTCTCTGGATGCCCTAGATGTCCATGTGGGTTCCAACATAGAAATTAAG 1884
Qy 460 TrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMet 479
Db 1885 TGGTCTCAGAGCTAGACGACGCGCAAAATGGAGGAGGAATTCGAGCATGTGTGGACAGA 1944
Qy 480 AsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIle 499
Db 1945 AATCTCTATATCGATTGCATATTGGATGTCACTCTACGAAAGCGCAGGGAATCGCAGGATA 2004
Qy 500 ValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyr 519
Db 2005 GTACTCAGTGTGTTTTCATCCAGATATCTGCATCTATTCAGATTTCAGACAAATCGATAC 2064
Qy 520 ProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArg 539
Db 2065 CTTGTCTATGTTCTTAATCTCGGACGACGCAAAATACAGAAATATATGACCCACG 2124
Qy 540 SerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsn 559
Db 2125 GGCAACTCCATGGAGCTGGCGGTGGCCACGCGTGGCCATGGAGTTCCTGGGTGTGTG 2184
Qy 560 ValHisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGly 579
Db 2185 GCACACACGAGACCTGCTGCGAGATCCCAAGTCCAGTGAATCTGCCAAGGAGCGTGA 2244
Qy 580 LeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLys 599
Db 2245 TTGGTGTCTGTTTGTGGGCGCAGCATACAACTCCAAAGGATACCATCAAGCTGTTAAAG 2304
Qy 600 GluLeuGlyValAsnGlyLeuIleTyrAspArg-----IleTyrAspTrpMetProGlu 617
Db 2305 GAACCTGGCTGACGCGCATCATCTACGACAAATATGATGTCCTGACCCACCAAGGAGGTC 2364
Qy 618 GlnProAsnIlePheGlnValGlu-----GlnLeuGluArgLeuLysGlnGlu 633
Db 2365 AAGCAAAAGTGTGTTCCACCTTCAGGCCCAAGACAGCCAAAGAACTGCTCAAGTTGCAG 2424
Qy 634 LeuProGluLeuLysSerCysLeu-----641
Db 2425 GCCCTGAAATGGG-GCATGTGTGGCACACCTCTCGCAGCGAAACGAGGACGACGAGC 2483
Qy 642 -----CysProThrValSerArgPheValProSerSerLeuCys 654
Db 2484 ATAGAATTTGAATATCGAACTGCTCGACTATT-----TTATACTCATCTTTATGT 2534

RESULT 4
US-11-097-143-5113/c
; Sequence 5113, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
```

; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5113
; LENGTH: 5439
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-5113

Alignment Scores:

Pred. No.:	4,11e-74	Length:	5439
Score:	922.00	Matches:	239
Percent Similarity:	49.00%	Conservative:	105
Best Local Similarity:	34.05%	Mismatches:	226
Query Match:	26.07%	Indels:	133
DB:	12	Gaps:	20

US-10-047-855-3 (1-672) x US-11-097-143-5113 (1-5439)

```
QY 14 LeuLeuProGlyGluValPheAlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsn 33
Db 3556 CTGGCGCCCAACAGCAGATTGGCCATAGTGGGTAATTGGAGCGCTGGGCAACTGGCAG 3497
QY 34 ProGlnAsnAlaValAlaLeuLeuPro---GluAsnAspThrGlyGluSerMetLeuTrp 52
Db 3496 CACTCGGAGCGCTATTGTTCAAAATAGAGGAGGACATGATGATGATGATGATGATG 3437
QY 53 LysAlaThrIleValLeuSerArgGlyValSerValGlnTrpArgTyrPheLysGlyTyr 72
Db 3436 ACAGGAGAGATCTATATTCGGCTGCTGTCACGCAATATGCTATATGCTGTC---TGT 3380
QY 73 PheLeuGluProLysThrIleGlyGlyProCysGlnValIleValHisLysTrpGluThr 92
Db 3379 GCGCTGCATCCC-----GGCAGGAGCAGCTGATTGTCGCGCTTGGGAAACG 3332
QY 93 HisLeuGln-----IleAspAspGlyGlnPheGlyIleHisAsnGlyVal 97
Db 3331 CAATTACAGGTTCCAAATTCATTATGTACTGACGACCCCTATACGATGATGATCCAAA 3272
QY 98 SerIleThrProLeuGluSerGluIleIle-----107
Db 3271 ATCCAGCTGACCTGGGATCGGATTTGATTGTATGCACTCGTATGCGATTCATGTTG 3212
QY 107 -----107
Db 3211 GAGCTAGCCCAATAACATTGCTAAGAGATTCCCTTTCTTACAGCCCGCAATAGTCAAGG 3152
QY 108 -----IleAspAspGlyGlnPheGlyIleHisAsnGlyVal 119
Db 3151 AGTTGATGAGCAGCCTGCCAAGAAATCAG-AGTGACATATTGGCTGTTCAATGCCAG 3093
QY 120 GluThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyr 139
Db 3092 GAGAAGGTGATCGGGCTGGCTGACCAAGGAGACTCTGTGTCAGCTAAAGTTCTTTTAT 3033
QY 140 SerGluLysProValSerIleThrLysLysLeuLysLysSerArgPheArgVal 159
Db 3032 GCT-----CCGTTCACTGTT---AAGCAGCGATGAACGTAGGATATCCAGGTC 2985
QY 160 LysLeuThrLeuGluGlyLeuGlu-----GluAspAspAspArgValSerProThr 177
Db 2984 AAGTGACCCCATGAACTGATATTCAGTGGCGGCTGTGATACCATGCTGCCCTCG 2925
QY 178 ValLeuHisLysMetSerAsnSerLeu-----186
Db 2924 -----TCTCCCATGGAGGATTCCTGTGCAACGACACTCATGATACCAAGGAGACGGC 2871
QY 187 -----GluIleSerLeuLysSerAspAsnGluPhe 196
Db 187 -----186
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Db 2870 GGTGAATCTCCACACCCCTTTGCTTTAGCGAGTCTGTCACCTTGAGTCCGCGACGAGTGC 2811
QY 197 LysCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGlu 216
Db 2810 GAAATCAGA--AGTCAAGAGCAGTTTCGGCACCCTGGAGCCACCGATTGGTTTATA 2754
QY 217 TyrSerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGlu 236
Db 2753 TTCCATCTGACCGTTGGAGACTTCGAGAAACACGCGCTACCTGATTGATTGTATC----- 2700
QY 237 AspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCys 256
Db 2699 AGCTACAGCTCCCGGTGGCCAGGAAGATGGTCCACCAACCACTTGGCTATCATAT 2640
QY 257 LeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIle 276
Db 2639 GTGCTGCCCAATCTTTTAA-----CGTTCTGAAGGCAACTTGGAGCTGCCCAT 2589
QY 277 MetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleLys 296
Db 2588 ACCTGTGCCAAGGGCCATCGACCTCTGGGAATGATGCTCTTGTGTTATCTTATCGTGAAG 2529
QY 297 ProLeuProGlyTyrSerCys-----AspMetLysSerSerPheSerLysTyrTrp 313
Db 2528 -----CCCTCATCGCTGTGCTCTAAATGGATATGAGTGTACGCTATGCCGATCTGG 2475
QY 314 LysProArg---IleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThr 332
Db 2474 AACAGCAAGTGGACGGGACTGGATGGGCCCATCTGTTCCGGAAGTACTAGT---TTCAAG 2418
QY 333 AlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHis 352
Db 2417 GCCAAGAGCGCTGTTATTCGGGAGATACCACTTCTTTGAAGAAATGGAAGTCTATCAC 2358
QY 353 GlyAlaAlaPheValGluPheAspValHisLysSerLysAspPheValProValValTyr 372
Db 2357 GGTGCGCAGATGGTGAGTTCGATGTCCAACTTAGCAAGATCTGTCGCGAGTGGTGTAT 2298
QY 373 HisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeu 392
Db 2297 CACGATTTCTATGATCTATCTTCACTAAAGTCCAGTCCAGTCCGAGGACGAGTTC 2238
QY 393 PheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHis 412
Db 2237 CTCGCTCTACCGATGAGGAGTGTCCCTGAGCAGTTCGAAGAAATGGAAGTCTATCAC 2178
QY 413 ValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGluGluAsnSerPhe 432
Db 2177 ATTGCT-----GAGGGTCTGTCCAGGAGACGCGTTCGTTT 2142
QY 433 Ser-----GluAsnGlnProPheProSerLeuLysMetValLeuGluSer 447
Db 2141 CACAACGATGATTGTTAGACACCGCGTTCGCGAGTATGCGATGCTCTGGATGCC 2082
QY 448 LeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnGlnArgAspGly 467
Db 2081 CTAGATGTCATGTGGGTTTCAACATAGAAATTAAGTGTCTCTCAGAGGCTAGAGGACGGC 2022
QY 468 MetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAspIleLeu 487
Db 2021 AAAATGGAGGAGGAATTCGAGCATGTGGGACAGAAATCTCTATATGATTCATATTG 1962
QY 488 LysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPheAspAlaAsp 507
Db 1961 GATGTCATCTCAGAAAGCAGGGAATCCAGGATAGTACTGATGTTGTTGATCCAGAT 1902
QY 508 IleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrGlnGly 527
Db 1901 ATCTGCACTATTCTGAGATTCAAGCAAAATCGATACCTGTCTATGTTCTTAATCTCGGC 1842
QY 528 LysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAlaMet 547
Db 1841 AGGACGACGAAATACCAAGATATATGGACCCCGGCAACTCCATGGAGCTGGCGCGTG 1782
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Qy 548 SerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuArg 567
Db 1781 TGGCAGCGGGTGGCCATGAGTTCTCGGTGTTGTGGCACACACGGAGGACCTCTCGGA 1722
Qy 568 AsnProSerTyrIle----- 572
Db 1721 GATCCCATGTCAGGTAAACATGATCCACTCTCGAATCGTGGAATCATTCAGCTACGACGCTT 1662
Qy 573 -----GlnGlu-AlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAspThrAs 590
Db 1661 TTAGTGATCTGGCCAGAGCGTGGATTGGTGTGTTTGGGGCGGACGATAACAA 1602
Qy 590 nAspProGluAsnArgArgLysLeuGluLeuGlyValAsnGlyLeuIleTyrAspAr 610
Db 1601 CTCCAAGGATACCATCAAGCTGTTAAAGGAACTCGGCCTGCACGCCATCATTCAGCAAA 1542
Qy 610 gile 611
Db 1541 AATG 1538

RESULT 5
US-11-097-143-27182
; Sequence 27182, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27182
; LENGTH: 2392
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-27182

Alignment Scores:
Pred. No.: 5.66e-51 Length: 2392
Score: 667.00 Matches: 201
Percent Similarity: 47.24% Conservative: 124
Best Local Similarity: 29.22% Mismatches: 230
Query Match: 18.86% Indels: 134
DB: 12 Gaps: 26

US-10-047-855-3 (1-672) x US-11-097-143-27182 (1-2392)
Qy 3 ProSerGlnValAlaPheGluIleArg-----GlyThrLeuLeuProGlyGluValPhe 20
Db 371 CCCACTCGGGGAGTTCAATGCGGTGGAGGTTCCCTCGGCGCGGAGGAGCGACTG 430
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40

Db 431 GGGCTTACCGGCGATGTGAAAGCCCTCGCGGAGTGGCAGCTGTCCAGAAAGTGTGGCTCTA 490
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 491 -----GAATCGTGGACGAGCTCAATGGCAGGCCACGGTGCCTTACGTCC 538
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 539 TGCGCGCAGCTGGAGTACGCG-----TACTTTGTCTACGTGAGGATCTCTCT 586
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 587 GGCTACAAGCAG-----ATCCGCGCTGTGGAAACCCATTTCAAGCCAGGTCCTCGGA 640
Qy 101 Pro----- 101
Db 641 CCCTGTACGGAGCTACAGTCCAGCCAGTTGGACGTCTCTGGTATTACGTCCGCAAACTCC 700
Qy 102 -----LeuGluSerGluIleIleLeuAsp----- 109
Db 701 GATCTAAAGCCGCGAGGTGCACCGCGCTGCTGAACCATGAGGCCATTTCTGCAGCTCAAG 760
Qy 110 -----AspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTrp 126
Db 761 TTCAATGGCGAGAAGATGTTTCCAAGTCCACGAC---ATCGAGACCTTTGAC----- 808
Qy 127 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro----- 144
Db 809 -----CCCCAGCAGCTCCAGCTGAGATTTGTGCCCGTGGAGAAGACCGCTGGCCTG 859
Qy 145 ---ValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLysLeuThrLeu 163
Db 860 CATGTGGGNGTACTCCAAACAGAGGTACGGCAAGAGCCAGCTGGAGCTGCACCTACTTTC 919
Qy 164 GluGlyLeuGluAspAspAspArgValSerProThrValLeuHisLysMetSer 183
Db 920 ---GGAGTGCCTCTACACCAAGGGGACATTGTTCATCTTTCACATCAGCTGCCCTGGAG 976
Qy 184 AsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro 203
Db 977 AGGATGATGAGAG-----CAGCATTCCGCTG 1003
Qy 204 GluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGlu 223
Db 1004 GAGTGC-----TACAGCATGTCCAAC----- 1024
Qy 224 ProAspAsnLeuGluLeuIlePheAspPheGluAspLeuSerGluHisValVal 243
Db 1025 -----GAACCTCTG----- 1033
Qy 244 GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAla 263
Db 1034 -----GGCAGTGCACCTCTGGTCACCTCGGACCTGACT 1066
Qy 264 GluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer---ArgAsnSerArg 282
Db 1067 -----GGCAGCGAGGAGTGTCTCCACCTGCGGATTAAGTCCGCAAGATCCAGAT 1117
Qy 283 LysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGlyTyrSer 302
Db 1118 GAGACCTTGGCCAGGCTGAGCTTCCCTATGTGCGGTGCAGGCTTACCGCTACTCGCGG 1177
Qy 303 CysAspMetLysSerSerPheSerLysTyrTrpLysProArgIlePro---LeuAspVal 321
Db 1178 CTAGACTTCAAGAACACCTTATGCTCAGTCTGGCCCAAGAGCTGCCCACTGGATGTG 1237
Qy 322 GlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsn 341
Db 1238 GGTCTGCTGGAAATGGCAAGAGT---TACATTGCAGACGCTCTCTCGGAAAGGAGAAC 1294
Qy 342 ThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal 361
Db 1295 ACTATCGCGTCTTCTCTGAGCGCCCATGAACATCAGCAGCATGATCGATGTTGGATGTC 1354

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QY 362 HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet 381
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1355 CATTTGACTGCTGATGGTGGCTGTGTGATTTATCAGGATTTCCGAGTCCGAACTGCTCCG 1414

QY 382 LysLysLysPheAspAlaAspProValGluLeuPheGluLeuProValLysGluLeuThr 401
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1415 CTGGCAAGCAGATCAGCCGCGCAGACCGAGTGTGTGTGATCAAGACATAAAC 1474

QY 402 PheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArg 421
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1475 TATGACTGCTCAAAAGGCTGGCATCTTCTGTGTATCGCA----- 1516

QY 422 LysGluSerValValGlnGluGluAenSerPheSer-----GluAenGln 436
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1517 -----GGCCAAGTGAGGAGTATCTCTCGCACACCGCGAGCCAGGATGGAACACCGC 1570

QY 437 ProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAenIle 456
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1571 ATATTCACCAAGCTGTGTGAGGTACTGGAGAGCTGCCAAGTCACTGGGCATTGATGTG 1630

QY 457 GluLeuLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAenLeuSerThrTyr 476
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1631 GAGATTAAGTGG---CCACAGCGTCCCGAGGCG---GGAGGATCAGAGGCTGAGCAACA 1684

QY 477 PheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAenSerGlyLys 496
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1685 ATCGACAAGAATCTTTCGCGCAGAGGTATCATCATCAGTATCCAGAAAGGCTGTGCG 1744

QY 497 ArgArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGln 516
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1745 AGACCGAATAATCTTCTCCAGCTTCGATGCTGATGTCACATGTCACGATGCTGAGGTTCAAGCAG 1804

QY 517 AsnLysTyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMet 536
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1805 AAGCTTTCCTCAGTGTATCTTCACGAGGAGACGAGAGTGGCAGCGGTTCCTCG 1864

QY 537 AspLeuArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAenLeuLeu 556
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1865 GATCTCGGAACACGGACCTTTATTCAGCGCGTAACAATGCTCAAGCTTTCGAGCTGGCT 1924

QY 557 GlyIleAsnValHisThrGluAspLeuLeu---ArgAsnProSer---TyrIleGlnGlu 574
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1925 GGCACAGCTCCACACCGCAGGACTTCTCGGCGAAATGCAATGCTGCGAAAA 1984

QY 575 AlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsn 594
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 1985 GCAAGGATCTGGCCAAATAGCTGTGATCTGGGCGCAGATTGCAACTCCAGGAGCGG 2044

QY 595 ArgArgLysLeuLysGluLeuValAsnGlyLeuIleTyrAspArgIleTyrAspTrp 614
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 2045 GTGAGTACTTACCCGGATCGGGCTACCGCCACGCTAGCATCGCAGTATCTCTTC 2104

QY 615 MetProGlu-----GlnProAenIlePheGlnValGlnGluLeu---ArgLeuLys 631
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 2105 ATGCGGAGGCAAGCGCA-AGCCTTCTTCAATCACCAGCATGATGATGCGCGGATCGC 2163

QY 632 GlnGluLeuProGluLeuLysSer 639
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 2164 GCGCCAGTCCGGATCTAAGAAAT 2187
```

RESULT 6

```
US-11-097-143-26897
; Sequence 26897, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
```

```
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26897
; LENGTH: 2457
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-26897
```

Alignment Scores:

```
Pred. No.: 5,87e-51 Length: 2457
Score: 667.00 Matches: 201
Percent Similarity: 47.24% Conservative: 124
Best Local Similarity: 29.22% Mismatches: 230
Query Match: 18.86% Indels: 134
DB: 12 Gaps: 26
```

US-10-047-855-3 (1-672) x US-11-097-143-26897 (1-2457)

```
QY 3 ProSerGlnValAlaPheGluIleArg-----GlyThrLeuLeuProGlyGluValPhe 20
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 436 CCACCTCTCGGGAGTCAATGTGCGGCTGGAGGTTCCCTCGCCCGCAGGAGCGAGCTG 495

QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 496 GGGCTTACCGCGGATGTGAAGCCCTCGCGAGTGGCAGCTGTCCAGAGAGTGTGGCTCTA 555

QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTyrLysAlaThrLysValLeuSerArg 60
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 556 -----GAATCGCTGCAGCAGCTCAACTGGCAGCCACGCTGGCGCTTCAGTCC 603

QY 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 604 TCCCGCCAGCTGGAGTACCGC-----TACTTGTCTACGTGGAGGATCTCTCT 651

QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 652 GGCTACAGCAG-----ATCCGCGTGGGAACCCATTTCAGCCAGGTCCTCGGGA 705

QY 101 Pro----- 101
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 706 CCCTGTACGGAGTACAGTCAGCCAGCTTGGAGCTTCTCGGTATTACGTGCGAACAATCC 765

QY 102 -----LeuGluSerGluIleIleIleAsp----- 109
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 766 GATCTAAAGCCGAGGTGCACCGCGCTGGCTGAACCATGAGGCCATTCTCGAGCTCAAG 825

QY 110 -----AspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTrp 126
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 826 TTCATGGGAGAAGATGTTCCAGTCCACGAC---ATCAGACCTTTGAC----- 873

QY 127 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro----- 144
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 874 -----CCCCAGCACGTCCAGCTGAAGATTGTGCCCGTGGAGAAGACCGCTGCGCTG 924

QY 145 ---ValSerIleThrLysLysLeuLysLysSerArgPheArgValLysLeuThrLeu 163
|||||:|:| |||||:|:| |||||:|:| |||||:|:|
Db 925 CATGTGGAGTACTCCAAACAGGAGTACGGCAAGAGCCAGCTGGAGCTGAGCTACTTTC 984
```


517 AnLysTyrProLeuPheLeuThrGlnGlyLysSerGluLeuTyrProGluLeuMet 536
1870 AACGCTTCCAGTGTATGTTCTCAGCAGGAGAGACGAGAGTGGCGCGCTTCCTG 1929
537 AspLeuArgSerArgThrProLeuAlaMetSerPheAlaGlnPheGluAsnLeuLeu 556
1930 GATCTCGAACACGGACCTTTATTGACGCCGTAAACAATGCTCAAGCTTTCGAGCTGGCT 1989
557 GlyLeuAsnValHisThrGluAspLeuLeu---ArgAsnProSer---TyrIleGlnGlu 574
1990 GGACAGCTCCACACCGCGGACTCTCTGGCGGAAATGCATCAGAAATGCTCGAAAA 2049
575 AlaLeuAlaLysGlyLeuValIlePheCysTyrGlyAspThrAsnAspProGluAsn 594
2050 GCCAAGGATCTGGCCAAATAGCTGTGATCTGGGGCGACGATTGCAACTCCAGAGGCGG 2109
595 ArgArgLysLeuLysGluLeuGlyValAsnGlyLeuLeuTyrAspArgIleTyrAspTyr 614
2110 GTGACGACTTCCACCGGATCGGGGTACCGCACCGTGTACGATCGAGTGTCTTC 2169
615 MetProGlu-----GlnProAsnIlePheGlnValGlnLeuGlu---ArgLeuLys 631
2170 ATGCGGAGGGCAGCGCGA-AGCTTCTTCAATCACCAGCCTGATGCGCGAGTTCG 2228
632 GlnGluLeuProGluLeuLysSer 639
2229 GGCCAGTGGCGGATCTAAGAAAT 2252

RESULT 7
US-11-097-143-26896
; Sequence 26896, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26896
; LENGTH: 7162
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-26896

Alignment Scores:
Pred. No.: 2,528-50 Length: 7162
Score: 667.00 Matches: 201
Percent Similarity: 47.24% Conservatives: 124
Best Local Similarity: 29.22% Mismatches: 230
Query Match: 18.86% Indels: 134
DB: 12 Gaps: 26

US-10-047-855-3 (1-672) x US-11-097-143-26896 (1-7162)

164 GluGlyLeuGluGluAspAspArgValSerProThrValLeuHisLysMetSer 183
985 ---GGAGTGGCCCTACACCAAGGGGACATTGCTCATCATCAGCTCGCCCTGGAG 1041
184 AsnSerLeuGluLeuSerLeuLeuSerAspAsnGluPheLysCysArgHisSerGlnPro 203
1042 AGGATGATGGAG-----CAGCATCTCCGCTTG 1068
204 GluCysGlyTyrGlyLeuGlnProAspArgTyrThrGluTyrSerIleGlnThrMetGlu 223
1069 GAGTGC-----TACAGCATGTCCAAC----- 1089
224 ProAspAsnLeuGluLeuPheAspPheGluGluAspLeuSerGluHisValVal 243
1090 -----GAACCTCTG----- 1098
244 GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerThrIleAla 263
1099 -----GGCAGTGCCTCTGTCACCTCGGACCTGACT 1131
264 GluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer---ArgAsnSerArg 282
1132 -----GGCAGCGAGGAGTGTCCACCTGCCGATTAGTCCGCAAGAATGCAGAT 1182
283 LysThrIleGlyLysValArgValAspTyrIleIleLeuLysProLeuProGlyTyrSer 302
1183 GAGACCTGGCCAGGCTGAGGCTTCCTATGTCGGGTGCAGCCTTACCGCTACTCGCGC 1242
303 CysAspMetLysSerSerPheSerLysTyrTyrLysProArgIlePro---LeuAspVal 321
1243 CTAGCTTCAAGAACACCTATGCTCACTACTGCGCCAGAGCTGCGCCACCTGGATGTG 1302
322 GlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsn 341
1303 GGTTCATCGTGGAAATGCGAAGT---TACATTGCAGACGCTCTCGGAAAGGAGAAC 1359
342 ThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal 361
1360 ACTATCGCTCTTCTGAGCGCCCATGAACATCAGCAGACATGATCGAGTTGGATGTC 1419
362 HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet 381
1420 CATTTGACTCTGCTGCTGTGCTGTGATTATCAGCATTTGCGAGTTCGGAAGTGGCTCG 1479
382 LysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThr 401
1480 CTGGGCAAGCAGATCAGCCCGCCAGACCTGGAGTACGTGTGATCAAGACATAAAC 1539
402 PheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArg 421
1540 TATGAGCTGCTCAAAAGGCTGGCATCTTCTGTGTATGCA----- 1581
422 LysGluSerValValGlnGluAsnSerPheSer-----GluAsnGln 436
1582 -----GGCCAAAGTGGAGGATATCCCTCGCACACCGCCGAGCGGATGGAACACCCG 1635
437 ProPheProSerLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIle 456
1636 ATATTCCCAACGCTGGTGGAGGTACTGGAGAGCTGCCAAGTCTGCGCATTTGATGTG 1695
457 GluIleLysTyrIleCysGlnGlnArgAspGlyMetTyrAspGlyAsnLeuSerThrTyr 476
1696 GAGATTAAAGTGG---CCACACGCTGGCAGGCG---GGAGGATCAGAGGCTGAGCAACA 1749
477 PheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLys 496
1750 ATCGACAAGAACTTCTTCCGCGACAAGGTGATTCATCAGGTGATCGAAGAGGGCTGGC 1809
497 ArgArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGln 516
1810 AGACCGATAATCTTCTCCAGCTTCTGATGCTGACATGTGCAGATGCTGAGGTTCAACGAG 1869

Qy	3	ProSerGlnValAlaIapheGluIleArg-----GlyThrLeuLeuProGlyGluValPhe	20
Db	4141	CCCACTCTCGGGAGATTCAATGTGCGGTGAGGTTCCCTTGGCCGCCGAGGAGCGACTG	4200
Qy	21	AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu	40
Db	4201	GGGCTTACCGCGCATGTAAAGCCCTCGGCGAGTGCGAGTGTCCAGAATGTGGCTCTA	4260
Qy	41	LeuProGlnAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg	60
Db	4261	-----GAATCGCTGGACGAGCTCAACTGGCAGGCCACGGTGGCCCTTCAGTCC	4308
Qy	61	GlyValSerValGlnTrpArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly	80
Db	4309	TGCGCGCCAGCTGGAGTACCGC-----TACTTTGTCTACGTGGAGGATCTCTCT	4356
Qy	81	GlyProCysGlnValIleValHleLysTrpGluThrHisLeuGlnProArgSerIleThr	100
Db	4357	GGCTACAGCAG-----ATCCGCCGTTTGGAAACCCATTTCAMGCCACAGTCCCTGGGA	4410
Qy	101	Pro-----	101
Db	4411	CCCTGTACGGAGCTACAGTCGAGCCAGTTCGACGTCTTCGGTATTACGTCGACAACTCC	4470
Qy	102	-----LeuGluSerGluIleIleIleAsp-----	109
Db	4471	GATCTAAAGCCGCGAGTGCACCGCGGTGGCTGAACCATGAGGCCATTCTGCAGCTCAAG	4530
Qy	110	-----AspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTrp	126
Db	4531	TTCAATGGCGAGAAGATGTTCCAAGTCCACGAC-----ATCGAGACCTTTGAC-----	4578
Qy	127	LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro-----	144
Db	4579	-----CCCCAGCACGTCACAGATTGTGCGCGTGGAGAGACCGCTGGCCCTG	4629
Qy	145	---ValSerIleThrLysLysLeuLysLysSerArgPheArgValLysLeuThrLeu	163
Db	4630	CATGTGGAGTACTCCAAACAGGAGTACGGCAAGCAGCAGCTGGAGCTGCAGCCTACTTTC	4689
Qy	164	GluGlyLeuGluAspAspAspAspValSerProThrValLeuHisLysMetSer	183
Db	4690	---GGAGTGCCCTACACCAAGGGGGAATGTCTATCTTCATCATCAGCTGCCGCTGGAG	4746
Qy	184	AsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro	203
Db	4747	AGGATGATGGAG-----CAGCACTTCCGCTTG	4773
Qy	204	GluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTrpSerIleGlnThrMetGlu	223
Db	4774	GAGTGC-----TACAGCATGTCCAAC-----	4794
Qy	224	ProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGluHisValVal	243
Db	4795	-----GAACTCCTG-----	4803
Qy	244	GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAla	263
Db	4804	-----GGCAGTGCCACTCTGTGTCACTCCGACCTCGGACCTGACT	4836
Qy	264	GluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer---ArgAsnSerArg	282
Db	4837	-----GGCACGGAGGAGTGCTCCACTGCCGATTAAGTCGGCCAGAATGCAAT	4887
Qy	283	LysThrIleGlyLysValArgValAspTrpIleIleIleLysProLeuProGlyTyrSer	302
Db	4888	GAGACCCTGGCCAGGCTGAGCTCCCTATGTCGCGGTGCAGCCTTACCGCTACTCGCCG	4947
Qy	303	CysAspMetLysSerSerPheSerLysTyrTrpLysProArgIlePro---LeuAspVal	321
Db	4948	CTAGACTTCAAGAACACTTATGCTACTTCTGCGCCCAAGAGCTGGCCCACTGGATGTG	5007

Qy	322	GlyHisArgGlyAlaGlyAenSerThrThrAlaGlnLeuAlaLysValGlnGluAen	341
Db	5008	GGTCATCGTGGAAATGGCAAGAGT---TACATTGCAGACGCTCTCGCGAAAGCGAGAAC	5064
Qy	342	ThrIleAlaSerLeuArgAenAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal	361
Db	5065	ACTATCCGGCTTTCTTGAGCGCCATGAACATCAGCAGACATGATCGAGTTGGATGTC	5124
Qy	362	HisLeuSerLysAspPheValProValProValTyrHisAspLeuThrCysCysLeuThrMet	381
Db	5125	CAITTGACTGCTGATGTGTGTGCTGTGATTTATACGATTTTCGAGCTGCGAACTGCTCCG	5184
Qy	382	LysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThr	401
Db	5185	CCTGGCAAGCAGATCAGCCGCCAGACCATCGAGTACGTGTGTGATCAAGAAGCAATAAC	5244
Qy	402	PheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArg	421
Db	5245	TATGAGCTGCTCAAAAGGCTGCGCATCTTCTCTGTGTATCGCA-----	5286
Qy	422	LysGluSerValValGlnGlnGluAenSerPheSer-----GluAenGln	436
Db	5287	-----GGCCAAAGTGAGGGAGTATCCCTCGCAACAACGCCAGCCAGGATGGAAACACCGC	5340
Qy	437	ProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIle	456
Db	5341	ATATTTCCCAAGCTGTGTGGAGGTACTGGAGAACTGCCCAAGTCACTGGCGCATGTATGTG	5400
Qy	457	GluIleLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyr	476
Db	5401	GAGATTAAAGTGG--CCACAGCGTCGCCAGGCG--GGAGGATCAGAGGCTGAGCAACA	5454
Qy	477	PheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAenSerGlyLys	496
Db	5455	ATCGCAAGAAGAACTTCTTCGCCGCAAGAGGTGATCCATCAGGTGATCCAGAAGGCGCTGTGGC	5514
Qy	497	ArgArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGln	516
Db	5515	AGACCGAATAATCTTCCACGCTTCGATGCTGACATGTGCAAGATGTGAGGTTCACAGCAG	5574
Qy	517	AsnLysTyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMet	536
Db	5575	AACGTCCTCCAGTGTATTTCTTCACGAGGAGAGAGCAAGAAGTGGCAGCGCTTCTCTG	5634
Qy	537	AspLeuArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAenLeuLeu	556
Db	5635	GATCTGCGAAACGCGACCTTTATTTGCAAGCCGTAACAATGCTCAAGCTTTCGAGCTGGCT	5694
Qy	557	GlyIleAsnValHisThrGluAspLeuLeu---ArgAsnProSer---TyrIleGlnGlu	574
Db	5695	GGCACAGCTCCACAGCCGAGGAGCTTCTGGGCGGAAAATGCATCAGAAATGCTGCGGAAA	5754
Qy	575	AlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAen	594
Db	5755	GCCAAAGATCTGGGCAAAATAGCTGTGATCTGGGGCGCACGATTGCACACTCCAAGGAGCGG	5814
Qy	595	ArgArgLysLeuLysGluLeuGlyIleValAsnGlyLeuIleTyrAspArgIleTyrAspTrp	614
Db	5815	GTGCAGTACTTACCACCGGATTCGGGGCTTACCGCCACAGTGTCTACGATCGCATGATCTCTTC	5874
Qy	615	MetProGlu-----GlnProAsnIlePheGlnValGlnLeuGlu---ArgLeuLys	631
Db	5875	ATCCCGGAGGGCAAGCGCGA-AGCCTTCTTCAATCACCCGCACTGATGCGCGGATTCGC	5933
Qy	632	GlnGluLeuProGluLeuLysSer	639
Db	5934	GGCCCAAGTGGCGGATCTAAGAAAT	5957

RESULT 8
US-11-09
; Sequen
; GENERA
; APPLI

```

; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27181
; LENGTH: 9667
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-27181

Alignment Scores:
Pred. No.: 3,78e-50 Length: 9667
Score: 667.00 Matches: 201
Percent Similarity: 47.24% Conservative: 124
Best Local Similarity: 29.22% Mismatches: 230
Query Match: 18.86% Indels: 134
DB: 12 Gaps: 26

US-10-047-855-3 (1-672) x US-11-097-143-27181 (1-9667)
QY 3 ProSerGlnValAlaPheGluIleArg-----GlyThrLeuLeuProGlyGluValPhe 20
Db CCCACTCTGGCGGAGTCAATGTGCGGTGGAGGTTCCTCCGCGCGGAGGAGCGACTG 6705
QY 21 AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db GGGCTTACCAGCGATGTGAAGCCCTCGGCGAGTGCAGCTGTCCAGAGTGTGGCTCTA 6765
QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db -----GAATCGCTGGACGAGCTCAACTGGCAGGCCACGGTGGCCCTTCAGTCC 6813
QY 61 GlyValSerValGlnTrpArgTrpPheLysGlyTrpPheLeuGluProLysThrIleGly 80
Db TGCGCGCAGCTGGAGTACCGC-----TACTTTGTCTACGTGGAGGATCTCTCT 6861
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db -----ATCCGCGGTGGGAACCCATTTTCAAGCCAGTCCCTGGGA 6915
QY 101 Pro----- 101
Db CCCGTACGAGCTACAGTGCAGCGCTTCGTGATTTACGTGGGACAACTCC 6975
QY 102 -----LeuGluSerGluIleIleAsp----- 109
Db GATCTAAAGCCGAGGTGCACCGCGGTGGTGTGAACCATGAGGCCATTTTCGACGCTCAAG 7035
QY 110 -----AspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTrp 126
Db -----ATCGAGACCTTTGAC----- 7083

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127 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro----- 144
7084 -----CCCGCAGCAGCTCCAGCTGAAGATTGTGCCGTGGAGAGACCGCTGGCCGTG 7134
145 ---ValSerIleThrLysLysLysLysSerArgPheArgValLysLeuThrLeu 163
7135 CATGTGGAGTACTCCAAACAGGAGTACGGCAAGAGCCGCTGGAGCTGCAGCTACTTTC 7194
164 GluGlyLeuGluAspAspArgValSerProThrValLeuHisLysMetSer 183
7195 ---GGAGTGCCTACACCAAGGGGACATTGTCATCTTTCACATCAGCTCGCGCTGGAG 7251
184 AsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro 203
7252 AGGATGATGGAG-----CAGCACTTCGCGCTTG 7278
204 GluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGlu 223
7279 GAGTGC-----TACAGCATGTCCCAAC----- 7299
224 ProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGluHisValVal 243
7300 -----GAATCTCTG----- 7308
244 GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAla 263
7309 -----GGCAGTGCCACTCTGCTGCTACCTCGGACCTGACT 7341
264 GluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer---ArgAsnSerArg 282
7342 -----GGCAGCGAGGAGTGTCCACTCCGATTAAGTCGGCGCAAGATGCGAT 7392
283 LysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGlyTyrSer 302
7393 GAGACCTGGCGGAGCTGAGGCTTCCTCTAAGTCGGGTGAGCTTACCGCTACTCGCG 7452
303 CysAspMetLysSerSerPheSerLysTyrTrpLysProArgIlePro---LeuAspVal 321
7453 CTAGACTTCAAGAACACTATGCTACTTGGCCCAAGAGCTGGCCCAACCTGGATGTG 7512
322 GlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsn 341
7513 GGTCACTCGTGAATATGCAAGAGT---TACATTGCAGACGCTCTCGCGAAGGAGAGAC 7569
342 ThrIleAlaSerLeuArgAsnAlaSerHisGlyAlaPheValGluPheAspVal 361
7570 ACTATCGCGTCTTCTTCGAGCGCCCATGAACATCAGCAGACATGATCGAGTTGATGTC 7629
362 HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet 381
7630 CATTTGACTGTGATGGTGTGCTGTGATTTATCAGCATTTTCGGACTCGCAACTGCTCCG 7689
382 LysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThr 401
7690 CCTGCAAGCAGATCAGCCGCCAGACCCAGCTGGAGTACGTGCTGCTCAAGACATAAAC 7749
402 PheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArg 421
7750 TATGAGTGTCTCAAAAGGCTGCGCATCTTCTGTGATCGCA----- 7791
422 LysGluSerValValGlnGluAsnSerPheSer-----GluAsnGln 436
7792 -----GGCAAGTGGAGGATATCCCTCGCAACACCGCCGAGGATGGAAACACCGC 7845
437 PropheProSerLeuLysMetValLeuGluSerLeuProGluAAspValGlyPheAsnIle 456
7846 ATATTCCCAACGCTGGTGGAGTACTGGAGAGCTGCCCAAGCTTGGGCTGATGTG 7905
457 GluIleLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyr 476
7906 GAGATTAAAGTGG---CCACAGCGTCCGACGGGC---GGAGGATCAGAGGCTGAGCAACA 7959
477 PheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLys 496

```

```
Db 7960 ATCGACAAAGTCTTTCGCCACAGGTGATCCATCATGATCCAGAAAGCGGTGTCGC 8019
Qy 497 ArgArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGln 516
Db 8020 AGACCGATAATCTCTCCAGCTTCGATCTGACATGTGCAGCATGCTGAGGTTCAGCAG 8079
Qy 517 AenLysTyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMet 536
Db 8080 AACGCTCTCCAGTATGTTCTCCAGCGGAGGAGACGAAAGAGTGGCAGCGCTTCCTG 8139
Qy 537 AspLeuArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeu 556
Db 8140 GATCTGCGAAACAGCACCTTTATTGACGCGGTAACAAATGCTCAAGCTTTTCAGCTGCT 8199
Qy 557 GlyIleAsnValHisThrGluAspLeuLeu---ArgAsnProSer---TyrIleGlnGlu 574
Db 8200 GGCAGAGCTCCACAGCCGAGGAGCTCTCGGCGGAATGCAATGCTGCGAATA 8259
Qy 575 AlaLysAlaLysGlyLeuValIlePheCysThrGlyAspAspThrAsnAspProGluAsn 594
Db 8260 GCCAAGGATCTGGGCAATAGCTGTGATCTGGGCGCAGATTGCAACTCCCAAGGAGCGG 8319
Qy 595 ArgArgLysLeuLysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrp 614
Db 8320 GTGCAGTACTTACCCCGGATCGGGGTACCGCCACGTCGTACGATCGCAGTGATCTCTTC 8379
Qy 615 MetProGlu-----GlnProAsnIlePheGlnValGlnLeuGlu---ArgLeuLys 631
Db 8380 ATCCCGAGGCGGCAAGCGCA-AGCTTCTTCAATACCCGCACTGATGGCGGAGTTGCG 8438
Qy 632 GlnGluLeuProGluLeuLysSer 639
Db 8439 GSCCCAGTCCGGATCTAAGAAAT 8462
```

RESULT 9

```
US-11-097-143-19967
; Sequence 19967, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19967
; LENGTH: 2299
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-19967
Alignment Scores:
Pred. No.: 6,646-51 Length: 2299
```

```
Score: 666.00 Matches: 177
Percent Similarity: 50.00% Conservative: 133
Best Local Similarity: 28.55% Mismatches: 250
Query Match: 18.83% Indels: 60
DB: 12 Gaps: 17
US-10-047-855-3 (1-672) x US-11-097-143-19967 (1-2299)
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 416 GCCCTGTGGGCAATCTCCAGTGTGGCGCTGCAAGCGGAGCGCTGTGCTCCTC 475
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 476 -----AACCGCACTGCAATCTGAATGTTGGAGCGCTCCGTGGAGATACGCAA 526
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 527 AACAGCAGCGTGTGATCTGCTACTTTGCCGCC-----CCGTTGGC 568
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 569 CAGAGTGGAGCGGTGCAGATTCCGCGCTGGGAGTGCATGTCCAGCAAGGACCTTAAAT 628
Qy 101 ProLeuGluSerGluIleIleLeaAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 629 ACCACCAAGTTTCAGTGGCAATCGCAGCGAT---GAGTTCCGACTCATTTGGCAATGAGCGC 685
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIle-----Arg 134
Db 686 CAGTTGTCCGCTGGCTGCTCAGGACTCGGGCAACATTCTGCAGTTGAAGCTCTTCCGC 745
Qy 135 LeuArgLeuHisTyrSerGluLysProValSerIleThrLysLysLysLeuLysLys 154
Db 746 GAGGCTCTGAGCTTGGAGAGCAACCGGAGGTGGGGCAGAGAGCTGCTGCGT--- 802
Qy 155 SerArgPheArgValLysLeuThrLeuGluGlyLeuGluAspAspAspArgVal 174
Db 803 -----TTGCAACCACTAGATCCAAAGACTCTTA 829
Qy 175 SerProThrValLeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsn 194
Db 830 GCGCC-----ATCCTAAGTTCCGACGTCCCAATGTGGAGTACGTGCGAATGGCGTACG 886
Qy 195 GluPheLysCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrp 214
Db 887 GACAGTAAGTGGG---GTGCAGCGGAGTACGAGTGCCCTACGCCACCGGTGACATC 943
Qy 215 ThrGluTyrSerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPhePhe 234
Db 944 CTCATGTTCCATGTGAACCTGGAACAGCTGGATCGAGTGGCGCTATCTGTTGGAAGTTAT 1003
Qy 235 GluGluAspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThr 254
Db 1004 GCCGAACCAACCGGATGAGGACCTGCTCGCT-----CTCTAGGATAC 1045
Qy 255 AlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeu 274
Db 1046 TCGCACCTGTGCACACCTCGTTC-----TCCGCG---ACTGAAGCGGATGTGTCATC 1096
Qy 275 ProfileMetSerArgAsnSerArgLysThrIleGlyLysValAlaValAspTyrIleIle 294
Db 1097 GACCTTATTTCCGCGCTCTGGCAGCGCTGGTGGGTCAACTCGCTATTGAGTACCTGCAC 1156
Qy 295 IleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTrpLys 314
Db 1157 ATTCGCGCCATGGAGAGGATGGCTTCGATCTGCCACACAGCTTCGCCAATCTACCTGCGC 1216
Qy 315 ProArg---IleProLeuAspValGlyHisArgGlyAlaGlyAsnSer---ThrThrThr 332
Db 1217 TCCAAATGGACAGCCCTGGAGATTGGCCATTGGGATTTGGGAAATCTCTTACGTTACCC 1276
Qy 333 AlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHis 352
```

```

; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19966
; LENGTH: 4299
; TYPE: DNA
; ORGANISM: DROSOPHILA
; US-11-097-143-19966

Alignment Scores:
Pred. No.: 1,56e-50      Length: 4299
Score: 666.00           Matches: 177
Percent Similarity: 50.00%      Conservative: 133
Best Local Similarity: 28.55%    Mismatches: 250
Query Match: 18.83%             Indels: 60
DB: 12                        Gaps: 17

US-10-047-855-3 (1-672) x US-11-097-143-19966 (1-4299)

Qy 21 AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 1416 GCCTGTGTGGCAATCTGCAGTCTGGCGGCTTGGCAAGCGGAGCGCTGTGCTCTC 1475
Qy 41 LeuProGlnAsnAspThrGlyGluSerMetLeuTrpLysAlaThrLeuValLeuSerArg 60
Db 1476 -----AACCCGACTGCAATCTGATGTTTGGAGCGCTCCGTGGAGATACCGCAA 1526
Qy 61 GlyValSerValGlnValIleValHisLysTrpGlnThrHisLeuGlnProArgSerIleThr 80
Db 1527 AACAGCAGCGTTGAGTATCGCTACTTTGCCGCC-----GCCGTTGGC 1568
Qy 81 GlyProCysGlnValIleValHisLysTrpGlnThrHisLeuGlnProArgSerIleThr 100
Db 1569 CAGAGTGAGCGCTGCAGATTCCGCCGCTGGAGTTCGATGTCAGGCAAGACCTTTAAT 1628
Qy 101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 1629 ACCACCAAGTTTCAGTGGCAATCGCAGCGAT---GAGTTCGGACTCATTTGGCAATGAGCGC 1685
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIle-----Arg 134
Db 1686 CAGTTGTCCGCTGGCTGGCTTCAGGACTCGGGCAACATTTGCGAGTTGAAGCTCTTCGC 1745
Qy 135 LeuArgLeuHisLysTrpSerGluLysProValSerIleThrLysLysLysLysLys 154
Db 1746 GAGGCTCTGAGCTGGAGGCAACCGGAGTGGGGCAGGAGAGAGCTCGCTCGCT--- 1802
Qy 155 SerArgPheArgValLysLeuThrLeuGluGlyLeuGluAspAspAspArgVal 174
Db 1803 -----TTGCAACCAAGTAGATCCAAAGACTCTA 1829
Qy 175 SerProThrValLeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsn 194
Db 1830 GCGCCC---ATCCTAAGTTCCGCACGTCGCAATGTGGAGTAGCTGCGAATGCGGTACCGT 1886
Qy 195 GluPheLysCysArgHisSerGlnProGluCysGlyTrpGlyLeuGlnProAspArgTrp 214
Db 1887 GACAGTAAGCTCGG---GTGCAGCGCGGAGTAGGAGTGCCCTACGCCACCGGTGCATC 1943
Qy 215 ThrGluTyrSerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPhe 234

```

```

RESULT 10
US-11-097-143-19966
; Sequence 19966, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05

```



```

Db 355 -----GATGAGGTGTATATACGCTTCTGGGAGTCCCAATATATATCCAGAGTG 402
Qy 99 IleThrProLeuGluSerGluIleIleAspGlyGlnPheGlyIleHisAsnGly 118
Db 403 ATTGAACCTTGTGAGACATCTCTGAGAACTGCGACGCTTTTGGAAAACACACGAGAT 462
Qy 119 ValGluThr-----LeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArg 136
Db 463 GATGAGCGAACACAGGTGATCGCGCTGGCCACACAGAGACAATTTGTGCACCTGAAG 522
Qy 137 LeuHisTyrSerGluLysProProValSerIleThrLysLysLysLysLysSerArg 156
Db 523 ATCTTC-----AATGCTCCATCTGTGTGGCAACGTCAGAAACCGAGGCTCCTGTAT 573
Qy 157 PheArgValLysLeuThrLeuGluLysLeuGluAspAspArgValSerPro 176
Db 574 GTCCATGTGCAACCCCATGTTGAGTGGCGGAGAAATCTTGTAGCAACACGCAATCCC 633
Qy 177 ThrValLeuHisLysMetSerAsnSerLeuGluIleSer-----LeuIleSerAspAsnGlu 195
Db 634 -----ATCAAAATGTTTCGTCGCAACACGCTTTATCGGTATCTCAGCACCGCGAA 687
Qy 196 PheLysCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThr 215
Db 688 ATTAGGCGAGGAACAGCATCTTCAA-----TTGGCAAGTCGAGGTGACC 735
Qy 216 GluTyrSerIleGlnThr-----MetGluPro 224
Db 736 AATCTATGTGTCAAAATGCTTTGGCGCGCGACGAACTTTGGAGCGAGATGGGCGG 795
Qy 225 AspAsnLeuGluLeuIle-----PheAspPheGluGluAspLeuSerGlu--- 240
Db 796 AAGGATATGGAGCTATTTCAATGTTCCATCGCTTTTCCGGAGGAAACGCTCTACCGACTG 855
Qy 241 -----HisValValGlnGlyAspAlaLeuProGlyHisValGlyThr 254
Db 856 GATTGTGTACATACGCGCATAAAGCAGCTATGATGAACACCGCTATCATTCAGGGTAC 915
Qy 255 AlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeu 274
Db 916 GGATTCCTGTCCAGATCAGCTGCTGGCGACCGAAGGCTCTGCCGGGTG----- 966
Qy 275 ProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIle 294
Db 967 AAGATCACTTGCCTCCACCCACCTCCACTAATGAGATGTGTACGCTATCTAATA 1026
Qy 295 IleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTrp--- 313
Db 1027 ATTCGACCTTTGCCAAATTTCCGTTCGATTTGAGCCACAGCTACGAGCGTTACTGGCGC 1086
Qy 314 LysProArgIleProLeuAspValGlyHisArgGlyValGlyAsnSerThrThrThrAla 333
Db 1087 AAAAATCGCTATGCTGAACATCGGGCAAAAGGATCGGGAAT-----ACGTAC 1137
Qy 334 GlnLeuAlaLys-----ValGlnGluAsnThrIleAlaSerLeuArgAsnAlaLaSer 351
Db 1138 CGGTTAGGATCCGATGTGTTAGGAGAAATACCTTGTATGTTCAAGCAGGCTGTTTG 1197
Qy 352 HisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValVal 371
Db 1198 GCCAATGCAGACATGGTGGAGATGATGTCAGCTCAGCAGGATGCCAGGTTGGTGGTG 1257
Qy 372 TyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProVal--- 390
Db 1258 TATCAGCATTTTGTACTGCGATTTATGTTGCAGAGAATGCTAGTTTGGAGTCTCTG 1317
Qy 390 ----- 390
Db 1318 GAGAAATCAGGATCTGCTGATATTTGCTACGAAATCTTAACAACTAATGCTCCTCGCT 1377
Qy 391 -----GluLeuPheGluIleProValLysGluLeuThrPheAsp 403

```

RESULT 12

```

US-11-097-143-40594
; Sequence 40594, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR APPLICATION NUMBER: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR APPLICATION NUMBER: 60/164,769

```



```
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40594
; LENGTH: 4220
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-40594
```

Alignment Scores:

```
Pred. No.: 4,41e-50 Length: 4220
Score: 661.00 Matches: 203
Percent Similarity: 45.54% Conservative: 119
Best Local Similarity: 28.71% Mismatches: 279
Query Match: 18.69% Indels: 106
DB: 12 Gaps: 24
```

US-10-047-855-3 (1-672) x US-11-097-143-40594 (1-4220)

```
QY 3 ProSerGlnValAlaPheGluLeuArgGlyThrLeuLeuProGlyGluValPheAlaIle 22
DB 1127 CCTCTCTGTAGTCTTT-----CACAGTTACTAAACGGTAATGATGTGGCCATT 1180

QY 23 CysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeuLeuPro 42
DB 1181 AGTGCAACTGTCCTCTCTTGAAACTGGATCCCAAGGAG--GTGTACATTTTGGCC 1237

QY 43 GluAsnAspThrGlyGluSerMetLeu-----TrpYsAlaThrIleValLeu 58
DB 1238 AAGAATGACTGCTATGCTAGCTGCCTATGCAATGCGCTCAGTTTGAGGCAAGCTTAGAGATA 1297

QY 59 SerArgGlyValSerValGlnTyrArgTyrPheLeuGlyTyrPheLeuGluProLysThr 78
DB 1298 CCGGTAAACATGCATCACCATCTCGTACTCGTCTGCTC-----GTATCCACGATCCGAGACG 1354

QY 79 IleGlyGlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSer 98
DB 1355 -----GATGAGGTGATATACGCTTCTGGGAGTCCCAATTATATCCAGAGTG 1402

QY 99 IleThrProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisGly 118
DB 1403 ATTCGAACCTTGTGCAACACATGCTGAAGAACTGCGACGCTTTTGGAAACACACACGACGAT 1462

QY 119 ValGluThr-----LeuAspSerGlyTyrLeuThrCysGlnThrGluIleArgLeuArg 136
DB 1463 GATGAAGCGAACCAGGTGATCGCGCTGGCCACCACCAAGCAATGTGCACCTGAAG 1522

QY 137 LeuHisTyrSerGluLysProValSerIleThrLysLysLysLysLysSerArg 156
DB 1523 ATCTTC-----AATGCTCCATCTGTTGCAACGTCAGAACCGAGGCTCCGTGAT 1573

QY 157 PheArgValLysLeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerPro 176
DB 1574 GTCCATGTGCAGCCCATGTTTTCAGGTGCGCGAGAACCTTGTAAACGAAACGACCAATCCC 1633

QY 177 ThrValLeuHisLysMetSerAsnSerLeuGluIleSer-----LeuIleSerAspGlu 195
DB 1634 -----ATCAAAATGTTTTCGCGCAACACAGCTTTATCCGTTATCTGAGCACCCCGGAA 1687

QY 196 PheLysCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThr 215
DB 1688 ATTAGGACGGGACCAACAGTATCTTCAA-----TTGGCAAAAGTCGAGGTGACC 1735

QY 216 GluTyrSerIleGlnThr-----MetGluPro 224
DB 1735 -----CAGTATCGACACCAAGG 2836
```

```
DB 1736 AATCTATGTGTCAAAAATCTTTTGGCGCGCGACGACGATTTGGACCGACAGATGTGGCGCG 1795
QY 225 AspAsnLeuGluLeuIle-----PheAspPhePheGluGluAspLeuSerGlu----- 240
DB 1796 AAGGATATGGAGCTATTTTCATTTTCCATCGCTTTTCCGAGGAGAAACGCTCTACCGACTG 1855
QY 241 -----HisValValGlnGlnGlyAspAlaLeuProGlyHisValGlyThr 254
DB 1856 GATTTGTACACATACGCGCATAAAGCAGCTATGATGAACACCGCTATCATTCACGGGTAC 1915
QY 255 AlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeu 274
DB 1916 GGATTCCTGATGCCAGATCAGCTGCTGGCCACCGAAGGCTCTGCCCGGTG----- 1966
QY 275 ProfileMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIle 294
DB 1967 AAGATCACTTGGCGCTCCACCCACCGTCCACTAAATGGAGATGTGTACGCTATCAATA 2026
QY 295 IleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTrp--- 313
DB 2027 ATTGACCTTTGCCAAATTTCCGTTTCGATTTGAGCCACAGCTACGAGGTTACTGCGCG 2086
QY 314 LysProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrThrAla 333
DB 2087 AAAAATCGCCTATGCAATCAATCGGCAACAAAGGATCGGAAAT-----ACGTAC 2137
QY 334 GlnLeuAlaLys-----ValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSer 351
DB 2138 CGTTTAGGATCCGATGTGTAAGGAGATACCTTGTATGTTTCAAGCAGGCTGTTTG 2197
QY 352 HisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValVal 371
DB 2198 GCCAATGCAGACATGCTGGAGATGATGTCCAGCTCACGAGGATCCCGAGGTGGTG 2257
QY 372 TyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProVal--- 390
DB 2258 TATCAGATTTTGTACTGCGATTTATGTTGACAGAAATCCCTAGTTTTCAGGATCTTCTG 2317
QY 390 ----- 390
DB 2318 GAGATCAGGATCTGCTGATATTTGCCTACGAAATCTTAAACAACTAATGCTCTCGCT 2377
QY 391 -----GluLeuPheGluIleProValLysGluLeuThrPheAsp 403
DB 2378 ATGGGAGGATCAAAACGAAACGACCTCATTCGCTTCCCTCGGAGCAATTTCTACGAT 2437
QY 404 GlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGlu 423
DB 2438 CAACTGAAGGAGGTGAAGGCTCTGCGATTCGCTGGCAGCAAGGCTGCGATAAG----- 2491
QY 424 SerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMet 443
DB 2492 -----TCCTGTGATCGAATGTGTGGAGAGCGGCCCTTTCCTCTGCTCTCGAC 2542
QY 444 ValLeu-----GluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIle 461
DB 2543 CTCTCTGATAGGAAATCTACCGTCGACATGGGCTTCTTAATCGAGATCAAGTGCGCG 2602
QY 462 CysGlnGlnArgAspGlyMetTrpAsp---GlyAsnLeuSerThrTyrPheAspMetAsn 480
DB 2603 CAGATGACCAATATATCGCGGTGGGAGAGCGGAGCTTTAAGCCCACTGCGATCGAAAC 2662
QY 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
DB 2663 TTCTATGGACACCATATTTGAGATTTTAAATAAGCTTGGAAAGGCGCATAGTC 2722
QY 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnHisLysTyrPro 520
DB 2723 TTTTGCAGCTTCGATCGCGACATCTGTGCGATGTTGCGTTTAAAGCAGAATGTATATCCC 2782
QY 521 Ile----LeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArg 539
DB 2783 GTGACTTTTACTGAGGATCCGCACTCGCGGTT-----CAGTATCGACACCAAGG 2836
```



```
Db 472 AGAGTGGCTGAATGCTGCAGACCTACGAGATCTACCGCTCCCGGCTCTGGACATCTTC 531
Qy 108 IleAspAspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTyrLeu 127
Db 532 GCGGAGCCCTACCCGCTCTCAGTGGCGGGGATTC---TATCTGGAAACCGGTTGGTTG 588
Qy 128 ThrCysGlnThrGluLeuArgLeuArgLeuHisTyrSerGluLysProProValSerIle 147
Db 589 CAGTACGAGTACGTGATAGACCTAAATTCCTCTGGCAGGATCATATTTGCTATTCTC--- 645
Qy 148 ThrLysLysLysLeuLysLysSerArgPheArgValLysLeuThrLeuGluGlyLeuGlu 167
Db 646 -----GGAATGGGAAGTAACGCCAAGTACCGGTTGATCTCTACACCGCTCAAT 693
Qy 168 GluAspAspAspArgValSerProThrValLeuHisLysMetSerAsnSerLeuGlu 187
Db 694 TTGATAGACGACACGATAT-----GAG 717
Qy 188 IleSerLeuIleSerAspAsnGluPheLysCysArg-His---SerGlnProGluCysG1 206
Db 718 GTCTCCAGATATGCTTACAATCAGTCATCGTTCCAGACCCAGAACCAACGCGAGTGGCG 777
Qy 206 TyrGlyLeuGlnPro-----AspArgTyrThrGluTyr----- 217
Db 778 TACACAAAGGCAACCATTTGTTCTTCGCGATTTACCAACCGCTGGACACC-TACAATGC 836
Qy 218 -----SerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPhePh 234
Db 837 CCTTCGCTGCTATTATATCAGGCATCAAGAGAT-----CTCCAGTTA----- 879
Qy 234 eGluGluAspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyTh 254
Db 880 -----TCCCTTGGAGAGCGGTACATATTTCCGGATCAATCAAGGCG----- 921
Qy 254 rAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLe 274
Db 922 -----AGTCGTGGGATTTTGCAGCT 941
Qy 274 uProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIle11 294
Db 942 CCCCATCTTTGTAGTTTACAAATTTGGCCATTTGGGAGATCAGCTTGCCATTTATTTGGT 1001
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Db 1002 GGTTCACCTATGCGAAAGTGGAGCGGGAATCTACGAGCCAGTTTCCATCACTACTG 1061
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Qy 332 rAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHi 352
Db 1122 ATCTTCA---ACGAGTCTTACGGAGAACACCATCGAAAGTATCTGGCAGTTCTGAAGGC 1178
Qy 352 sGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTy 372
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Db 1239 GCATGATTTGGATTTTACACCTCAGACACAGATCGCTCTGTAAGGATCGCTTTGATTT 1298
Qy 392 uPheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHi 412
Db 1299 ACGTTTGTGCTAATAAGGAACCTTACCTACTCGAA-----CTCAAGCCCGCCGCG 1349
Qy 412 sValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGluAsnSerPh 432
Db 1350 GGTGTTATCTCTC-----AAACGTTGGACGCTCCAGGATACACCAATCT 1394
Qy 432 eSer-----GluAsnGlnProPheProSerLeuLysMetValLeuG1 446
Db 446 -----GluAsnGlnProPheProSerLeuLysMetValLeuG1 446
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Qy 446 uSerLeuProGluAspValGlyPheAsnIleGluIleLysTyrIleCysGlnGlnArgAs 466
Db 1455 GGCCTTACCACAAACACTGGGACTTCTGGTGGAGATTAAGTGG-----CCGCAAT-AA 1507
Qy 466 pGlyMetTyrAspGlyAsnLeuSerThrTyrPheAspMet-AsnLeuPheLeuAspIleI 486
Db 1508 TGGCTTCTGTGTGCGGAATCCACCAGAGTTTGAACAAAAACATTTAGCTGGACAGAA 1567
Qy 486 leLeuLysThrValLeuGluAsnSerGlyLysArgIleValPheSerSerPheAspA 506
Db 1568 TTTACAGATCAGATTCATCATGGGTGTGAGACCTCACTAATCTTCGCAGCTTTGATG 1627
Qy 506 laAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrG 526
Db 1628 CGGATATATGCACAAATGATTAGGCTGAGCAGCATGTCTCCCTGTGATTCTGATGAGCA 1687
Qy 526 lncGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleA 546
Db 1688 TTGGCAAGTCTCAGATTTGGGATGATATATGATCTGAGGGCACAGAGTTCCAGCAAG 1747
Qy 546 laMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnValHisThrGluAspLeuL 566
Db 1748 CCATCAACTCGTTCAGTCCGACAGAAATTTTGGAAACAGCTCTGCACGTGGAAACTTCC 1807
Qy 566 euArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTyrG 586
Db 1808 AAAACAAACACCGCAAGTCACTTGGCTTGGATGTGAGCAGTCTCTTTTATGCGG 1867
Qy 586 lyAspAspThrAsnAspProGluAsnArgArgLysLysLeuGlyValAsnGlyL 606
Db 1868 GTAACCATATGCAAGATGAACATCTTCTGGAGCAATTTAGAGCTCTGGATGTGACGGGTC 1927
Qy 606 eulleTyrAspArgIle-----TyrAspTyrMetProGluGlnProAsnI 621
Db 1928 TGATTTTACCATCATCGATGAGTGGGTCCGTTCCGTTGG-----AAACGATCCGAAT 1981
Qy 621 lePheGlnValGluGlnLeuGluArgLeu 630
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RESULT 15

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US-11-097-143-33685
; Sequence 33685, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33685
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; LENGTH: 4100
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-33685

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Score: 550.00 Matches: 182
Percent Similarity: 44.85% Conservative: 110
Best Local Similarity: 27.96% Mismatches: 261
Query Match: 15.55% Indels: 100
DB: 12 Gaps: 21

US-10-047-855-3 (1-672) x US-11-097-143-33685 (1-4100)
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QY 34 ProGlnAsnAlaValAlaLeuLeuProGlnAsnAspThrGlyGluSerMetLeuTriPhys 53
DB 1316 CTCGAGAGGCTCTACCCCTCAAGGAGCAGGACAGGCGCCACCAAGTGTATCTGAGG 1375
QY 54 AlaThrIleValLeuSerArgGlyValSerValGlnTyrArgTyrPheIysGlyTyrPhe 73
DB 1376 GTTGGATATGCCCGCCAGCCAG-----AGATTCTACTACCGATACCTG 1417
QY 74 LeuGluProIysThrIleGlyProCysGlnValIleValHisIleSlystrIleThrHis 93
DB 1418 ATATACTCCAAGAACAGACAGAGC-----AATCGGGTCTCGAGACCTGGGAGGCCAG 1471
QY 94 LeuGlnProArgSerIleThrProLeuGlu-----SerGluIlele 107
DB 1472 AGAGTGGCTCGATGCTGCAGACCTACGAGATCTACCGCTCCCGGGTCTGGACATCTTC 1531
QY 108 IleAspAspGlyGlnPheGlyIleHisAsnGlyValGluThrLeuAspSerGlyTriPhe 127
DB 1532 GCGGAGCGCTACCCGCTCTCAGTGGCGGGGATTTC---TATCTGGAACGCGTGGTGTG 1588
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DB 1589 CAGTACGAGTACGTGATAGACATAAATTCGCTGGCAGATCATATCTATTCT---1645
QY 148 ThrLysIleLysLeuLysIleSlySerArgPheArgValLysLeuThrLeuGluGlyLeu 167
DB 1646 -----GGAATGGGAAGTAACGCCAAGTACCGGTGTGATCTTACACGCTCAAT 1693
QY 168 GluAspAspAspArgValSerProThrValLeuHisIleSlyMetSerAsnSerLeuGlu 187
DB 1694 TTGATAGACGACACAGCTATT-----GAG 1717
QY 188 IleSerLeuIleSerAspAsnGluPheLysCysArg-His---SerGlnProGlyCysG 206
DB 1718 GTCTCCAGATATGCTCAATCATGATCATCTTCAGACCAACAGAACCAACCGGAGTCCG 1777
QY 206 YTyrglyLeuGlnPro-----AspArgTriPThrGlyTyr-----217
DB 1778 TACACACAGGCACCATTTGTTCCTCCGGATTACCAACCGCTGGACACC-TACAATGC 1836
QY 218 -----SerIleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPhePh 234
DB 1837 CCTTCGCTTGTCTATTATCAGGCATCAAGAGAT---CTCCAGTTA-----1879
QY 234 eGluGluAspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyTh 254
DB 1880 -----TCCCTTCGAGAGGCGGTACATATTTCCGGATCAATCAAGGCC-----1921
QY 254 rAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLe 274
DB 1922 -----AGTCGTGGGATTTTGCAGCT 1941
QY 274 uProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleI 294

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DB 2002 GGTTCACCTATGCGCAAAAGTGAGCGCGGGAATCTACAGCGAGTTTCCATCACTACTG 2061
QY 313 pLysProArgIlePro---LeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrTh 332
DB 2062 GCGGATATTTGGCCACATTTGGATGTGGATACCGAGGTTTGGAGCCAGCTACTTCCA 2121
QY 332 rAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaSerHi 352
DB 2122 ATCTTCA---ACGAGTCTTACGAGAACACCATCGAAAGTTATCTGGCAGTTCTGAAGGC 2178
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QY 412 sValThrAlaLeuLysSerLysAspArgLysGluSerValValGlnGluGluAsnSerPh 432
DB 2350 GGTGTTTATCTCTC-----AAACGTTGACCGTCCAGGAATACACCAATCT 2394
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QY 621 lePheGlnValGluGlnLeuGluArgLeu 630
DB 2982 TTTTCCGGCCCCACCAACTTATGAACATA 3010

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Search completed: July 3, 2005, 13:08:50
Job time : 1006 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 09:24:15 ; Search time 1063 Seconds
(without alignments)
3965.106 Million cell updates/sec

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Perfect score: 3537
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Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Published Applications NA -QFMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -LOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10047855 @CGN 1 1 740 @runat_01072005.155531_2380
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA:
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26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3537	100.0	2019	21	US-10-772-636-25	Sequence 25, Appl
2	3537	100.0	3206	16	US-10-047-855-4	Sequence 4, Appl
3	3537	100.0	3206	17	US-10-426-776-34	Sequence 34, Appl
4	3537	100.0	3265	21	US-10-887-553A-1007	Sequence 1007, Ap
5	3537	100.0	3499	10	US-09-814-353-21000	Sequence 21000, A
6	3537	100.0	3499	20	US-10-357-930-23730	Sequence 23730, A
7	3537	100.0	3499	20	US-10-357-930-23632	Sequence 29632, A
8	2965.5	83.8	3381	17	US-10-426-776-39	Sequence 39, Appl
9	2552	72.2	2738	17	US-10-426-776-32	Sequence 32, Appl
10	1399	39.6	2393	17	US-10-426-776-48	Sequence 48, Appl
11	824	23.3	471	9	US-09-998-598-1849	Sequence 1849, Ap
12	717	20.3	520	10	US-09-814-353-16669	Sequence 16669, A
13	698	19.7	436	9	US-09-796-692-8067	Sequence 8067, Ap
14	698	19.7	436	14	US-10-040-862-8067	Sequence 8067, Ap
15	698	19.7	436	17	US-10-057-475B-8067	Sequence 8067, Ap
16	698	19.7	436	17	US-10-154-884B-8067	Sequence 8067, Ap
17	698	19.7	436	19	US-10-764-324-8067	Sequence 8067, Ap
18	628	17.8	396	10	US-09-814-353-3977	Sequence 3977, Ap
19	628	17.8	396	10	US-09-814-353-10285	Sequence 10285, A
20	570	16.1	425	20	US-10-357-930-35883	Sequence 35883, A
21	570	16.1	425	20	US-10-357-930-44946	Sequence 44946, A
22	564	15.9	327	20	US-10-357-930-15054	Sequence 15054, A
23	482.5	13.6	3672	17	US-10-369-493-46175	Sequence 46175, A
24	472.5	13.4	359	20	US-10-357-930-5885	Sequence 5885, Ap
25	432	12.2	3799	17	US-10-369-493-26821	Sequence 26821, A
26	430.5	12.2	2226	17	US-10-369-493-36472	Sequence 36472, A
27	347	9.8	193	9	US-09-864-761-31597	Sequence 31997, A
28	343	9.7	463	9	US-09-864-761-2380	Sequence 2380, Ap
29	339	9.3	1121	14	US-10-198-846-11446	Sequence 11446, A
30	304.5	8.6	1540	20	US-10-425-115-168092	Sequence 168092, A
31	299	8.5	1499	19	US-10-437-963-16440	Sequence 16440, A
32	298.5	8.4	1410	18	US-10-425-114-27639	Sequence 27639, A
33	298	8.4	1391	18	US-10-425-114-22987	Sequence 22987, A
34	291	8.2	401	9	US-09-864-761-15483	Sequence 15483, A
35	286.5	8.1	1596	18	US-10-425-114-31409	Sequence 31409, A
36	286.5	8.1	1724	20	US-10-425-115-162869	Sequence 162869, A
37	282	8.0	1399	18	US-10-425-114-22946	Sequence 22946, A
38	282	8.0	1637	20	US-10-425-115-168094	Sequence 168094, A
39	273	7.7	1523	18	US-10-425-114-22914	Sequence 22914, A
40	273	7.7	1604	20	US-10-425-115-34867	Sequence 34867, A
41	272.5	7.7	1949	20	US-10-739-930-755	Sequence 755, App
42	271.5	7.7	1164	19	US-10-437-963-96985	Sequence 96985, A
43	259	7.3	323	9	US-09-728-445-622	Sequence 622, App
44	255	7.2	151	9	US-09-864-761-19114	Sequence 19114, A
45	251.5	7.1	1191	19	US-10-437-963-22646	Sequence 22646, A

ALIGNMENTS

RESULT 1
US-10-772-636-25
; Sequence 25, Application US/10772636
; Publication No. US20050042687A1
; GENERAL INFORMATION:
; APPLICANT: Kelly, Louise M.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Farlow, Deborah
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 9118, 990, 17662, 81982, 630,
; TITLE OF INVENTION: 21472, 17692, 19290, 21620, 21689, 28899, 53659, 64549,
; TITLE OF INVENTION: 9465, 23544, 7366, 27417, 57259, 21844, 943, 2061, 5891,
; TITLE OF INVENTION: 9137, 13908, 14310, 17600, 25584, 27824, 28469, 38947,
; TITLE OF INVENTION: 53003, 965, 56639, 9661, 16052, 1521, 6662, 13913, 12405 OR
; TITLE OF INVENTION: 5014

FILE REFERENCE: MPI03-015P1RNMNIM
CURRENT APPLICATION NUMBER: US/10/772.636
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US 60/445,241
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/448,389
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/456,320
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/460,279
PRIOR FILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: US 60/465,924
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/470,052
PRIOR FILING DATE: 2003-05-13
PRIOR APPLICATION NUMBER: US 60/498,106
PRIOR FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: US 60/500,179
PRIOR FILING DATE: 2003-09-04
PRIOR APPLICATION NUMBER: US 60/502,909
PRIOR FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: US 60/510,351
PRIOR FILING DATE: 2003-10-10
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 80
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 2019
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2019)
US-10-772-636-25

Alignment Scores:
Pred. No.: 0 Length: 2019
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-10-047-855-3 (1-672) x US-10-772-636-25 (1-2019)

Qy	1	MetThrProSerGlnValAlaPheGluLeuArgGlyThrLeuLeuProGlyGluValPhe	20
Db	1	ATGACACCTTCTCAGGTTGCTTGAATAAGAGGAACTCTTTTACAGGAGAGTTT	60
Qy	21	AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu	40
Db	61	CGGATATGTGGAGCTGTGATCTTTGGGAACTGGAATCCTCAAAATGCTGTGGCTCT	120
Qy	41	LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg	60
Db	121	CTTCCAGAGAATGACACAGGTGAAGCATGCTATGGAAGCAACCATTTGACTCAGTAGA	180
Qy	61	GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly	80
Db	181	GGAGTATCAGTTCAGTATCGCTACTTCAAAGGGTACTTTTAGAACCAAGACTATCGGT	240
Qy	81	GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr	100
Db	241	GGTCCATGTCAAGTGATAGTTACAGTGGGAGACTCATCTACAACCAACCATCAATAACC	300
Qy	101	ProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu	120
Db	301	CCTTTAGAAAGCGAAATTTATTGACGATGCACAAATTTGGAATCCCAATGTGTGAA	360
Qy	121	ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer	140
Db	361	ACTCTGGATTCTGGATGCTGACATGTCAAGTGAATGATTTACGTTTGCATTATCT	420

Qy	141	GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys	160
Db	421	GAAGAACCTCTGTGTCAATAACCAAGAAAAATTAATAATCTAGATTTTAGGTGAAG	480
Qy	161	LeuThrLeuGluGlyLeuGluAspAspAspArgValSerProThrValLeuHis	180
Db	481	CTGACACTAGAAGGCTCGAGGAAGATGACGATGATAGGGGTATCTCCCACTGTACTCCAC	540
Qy	181	LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis	200
Db	541	AAATGTCCAATAGCTTGGAGATATCTTAAATAGGACAAATGAGTTCAAGTGCAGGCAT	600
Qy	201	SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln	220
Db	601	TCACAGCCGGAGTGTGTTATGGCTTGCAGCCTGATCGTTGGACAGATACAGCATACAG	660
Qy	221	ThrMetGluProAspAsnLeuGluLeuPheAspPhePheGluGluAspLeuSerGlu	240
Db	661	ACGATGGAAACAGATAACCTGGAACTAATCTTTGATTTTTTGAAGAAATCTTCAGTGAG	720
Qy	241	HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer	260
Db	721	CACGTAGTTCCAGGATGATGCCCTTCTGGACATGTGGTACAGCTGTCTTATCATCC	780
Qy	261	ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn	280
Db	781	ACCATTGTCTGAGATGGAAAGAGTGTGGAAATCTTACTCTTCCCATCATGACAGCAAAAT	840
Qy	281	SerArgLysThrIleGlyLysValArgValAspTyrIleIleLeuLysProLeuProGly	300
Db	841	TCCCGGAAACCAATAGCAAGTGAAGTGTGACTATATAATTTAAGCCATTACACAGGA	900
Qy	301	TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp	320
Db	901	TACAGTTGTGACATGAATCTTCAATTTCCAGTATTGGAGCCCAAGAAATACCATTTGAT	960
Qy	321	ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu	340
Db	961	GTTGGCCATCGAGTGCAGGAAACTCTACAACAACCTGCCAGCTGGCTAAAGTTCAAGAA	1020
Qy	341	AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp	360
Db	1021	AATACTATTGCTTCTTTAAGAAATGCTGCTAGTATGCTGAGCTTTGTAGAAATTTGAC	1080
Qy	361	ValHisLeuSerLysAspPheValProValTyrHisAspLeuThrCysCysLeuThr	380
Db	1081	GTACACCTTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACTGTGTTGACT	1140
Qy	381	MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu	400
Db	1141	ATGAAAAAGAAATTTGATGCTGATCCAGTTCAATTTATTTGAAATTTCCAGTAAAAAGAAATTA	1200
Qy	401	ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp	420
Db	1201	ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACATAAATCAAGAT	1260
Qy	421	ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer	440
Db	1261	CGGAAGAAATCTGTGGTTCAGAGGAAATTTCTTTTCAGAAATCAGCCATTTCTTCT	1320
Qy	441	LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp	460
Db	1321	CTTATAGATGTTTATAGAGTCTTTGCCAGAGAGATGTAGGGTTTAAACATTTGAAATAAATGG	1380
Qy	461	IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn	480
Db	1381	ATCTGCCAGCAAGGATGGAATGTGGATGTGTAATCTTATCAACATATTTTTCACATGAAT	1440
Qy	481	LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal	500
Db	1441	CTGTTTTTGGATATATTTTAAAAACTGTTTTAGAAAAATTTCTGGGAGAGGAGATAGTG	1500
Qy	501	PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro	520

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Db 1501 TTTTCTTCATTTGATGCATATTTTCACAAATGGTTTCGCAAAAGCAGAACAAATATCCG 1560
Qy 521 IleLeuPheLeuThrGlnGlySerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1561 ATACTATTTTAACTCAAGGAAATCTGAGATTATCTCTGAACTCATGGACCTCAGATCT 1620
Qy 541 ArgThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
Db 1621 CGGACAAACCCCATTCGAATGAGCTTTGCACAGTTTGAATACTACTGGGGATAAATGTA 1680
Qy 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaIysAlaIysGlyLeu 580
Db 1681 CATACTGAAGACTTGCTCAGAAACCCATCTATATTCAAGAGCGCAAAAGCTAAGGGACTA 1740
Qy 581 ValIlePheCysTrpGlyAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1741 GTCATATCTCTGGGGTGTATGATACCAATGATCTCTGAAAACAGAGGAATTTGAAGGA 1800
Qy 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 1801 CTTGGAGTTAATGGTCTAATTTATGATAGATATATGATTTGGATGCTGAACCAACCAAT 1860
Qy 621 IlePheGlnValGluGlnLeuArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
Db 1861 ATATTCCAAAGTGAGCAATTTGGAACGCCCTGAAGCAGGAATTTGCCAGAGCTTAAGAGCTGT 1920
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 1921 TTGTGTCCACACTGTAGCCGCTTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 1980
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 1981 GTGGATGCCAACGGCATTGATAACGTGGAGAAATGCT 2016
```

RESULT 2

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US-10-047-855-4
; Sequence 4, Application US/10047855
; Publication No. US20030165863A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Lillian Wei-Ming
; TITLE OF INVENTION: NARC10 and NARC16, Programmed Cell
; DEATH OF INVENTION: Death-Associated Molecules and Uses Thereof
; FILE REFERENCE: 35800/242056
; CURRENT APPLICATION NUMBER: US/10/047,855
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/262,306
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3206
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)...(2163)
; NAME/KEY: misc.feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: Vector sequence
US-10-047-855-4
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Alignment Scores:
Pred. No.: 0 Length: 3206
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0
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US-10-047-855-3 (1-672) x US-10-047-855-4 (1-3206)

Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20

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Db 145 ATGACACCTTTCAGGTTGCCTTTTGAATAAGAGGAATCTTTTACCAGGAGAGTTTTT 204
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 205 GCGATATGTGGAGCTGTGATGCTTTGGGAAACTGGAACTCTCAAAATGCTGTGGCTCTT 264
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 265 CTTCCAGAGAAATGACACAGGTGAAAGCATGCTATGGAAGCAACCACTTGTACTCAGTAGA 324
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 325 GCGATATCAGTTTCAGTATCGCTACTTCAAAAGGGTACTTTTATAGAACCAAAAGACTATCGGT 384
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 385 GGTCCATGTCAAGTGTAGTTTCAAGTGGGAGACTCATCTACACACCACGATCNATAACC 444
Qy 101 ProLeuGluSerGluIleIleLeuAspAspGlyGlnPheGlyIleHisGlnGlyValGlu 120
Db 445 CCTTTAGAAAAGCGAAATATTATTGACGATGACAAATTTGGAATCCACAATGGTGTGAA 504
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Db 505 ACTCTGGATTCTGGATGGCTGACATGTGACACTGAAATTAAGATTACGTTTGCATTATCT 564
Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Db 565 GAAAACCTCTCTGTGTCAATAACCAAGAAAATAATTAATAAATCTAGATTAGGGTGAAG 624
Qy 161 LeuThrLeuGluGlyLeuGluAspAspArgValSerProThrValLeuHis 180
Db 625 CTGACACTAGAAAGGCTGGAGGAAGTACGATGATAGGGTATCTCCCACTGTACTCCAC 684
Qy 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
Db 685 AAAATGTCCAATAGCTTGGAGATATCTTAATAAGCGCAATGAGTTCAAGTGCAAGCAT 744
Qy 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
Db 745 TCACAGCCGAGTGTGGTTATGGCTTCAGACCTGATCGTTGGACAGAGTACGATACAG 804
Qy 221 ThrMetGluProAspAsnLeuGluIlePheAspPhePheGluGluAspLeuSerGlu 240
Db 805 ACGATGGAACACAGATAAACCCTGGAATAATCTTTTGAAGAAAGATCTCAGTGAG 864
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 865 CACGTAGTTTCAGGGTGATGCCCTTCTCGACATGTGGGTACAGCTTGTCTTATCATCC 924
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
Db 925 ACCATTGTGAGAGTGGAAAGAGTGTGGAATCTTACTCTTCCCATCATGAGCAAAAT 984
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
Db 985 TCCCGGAAAAACAATAGGCAAGTGGAGTTGACTATATAATTTATTAAGCCATTACCAGGA 1044
Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
Db 1045 TACAGTTGTGACATGAAATCTTCAITTTCCAAAGTATTGGAAGCCCAAGAAATACCATTTGGAT 1104
Qy 321 ValGlyHisArgGlyValAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 1105 GTTGCCCATCGAGGTGCAGAAACTCTACAAACATGCCAGCTGGCTAAGATTCAAGAA 1164
Qy 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyValAlaPheValGluPheAsp 360
Db 1165 AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCTATGTTGGTGCAGCCTTGTAGATTGAC 1224
Qy 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
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1225 GTACACCTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGACT 1284
Db
381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluLeuProValLysLysGluLeu 400
Qy
1295 ATGAAAAGAATAATTGATGCTGATCCAGTTCGAATTAATTGAAATTTCCAGTAAAGAATTA 1344
Db
401 ThrPheAspGlnLeuGlnLeuLysLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Qy
1345 ACATTGACCAACTCCAGTTGTAAAGCTCACTCATGTGACTGCAGCTGAAATCTTAAGAT 1404
Db
421 ArgLysGluSerValValGlnGluLeuAsnSerPheSerGluAsnGlnProPheProSer 440
Qy
1405 CGAAAGAATCTGTGGTTCAGAGGAAATTCCTTTTCGAAATTCAGCAATTCCTTCT 1464
Db
441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluLysTyr 460
Qy
1465 CTTAAGATGTTTATAGATCTTTGCGCAGAGATGTAGGTTTAACTTGAATTAATAATGG 1524
Db
461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Qy
1525 ATCTGCCAGCAAGGATGGAATGTGGATGGTAACTTATCAACATATTTTGACATGAAT 1584
Db
481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
Qy
1585 CTGTTTTCGATATAATTTTAAAACTGTTTGTAGAAATTCGGAGAGGAGATAGTATG 1644
Db
501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Qy
1645 TTTTCTTCATTGATGCAGATATTCACAATGGTTGCGCAAAAGCAAGCAAAATATCCG 1704
Db
521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Qy
1705 ATACTATTTTAACTCAAGCAAAATCTGAGATTTATCTCTGAACTCATGCACTCAGATCT 1764
Db
541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGluLysIleAsnVal 560
Qy
1765 CGGACAAACCCCAATTCGAATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATTAATGTA 1824
Db
561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Qy
1825 CATACTGAAGACTTGCTCAGAAACCCATCTTATATTCAGAGGCAAAAGCTAAGGGACTA 1884
Db
581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLysGlu 600
Qy
1885 GTCATATTCCTGCTGCTGGTGTATGATCAATGATCTCTGAAACAGAGAAATTTGAAGGAA 1944
Db
601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Qy
1945 CTTGGAGTTAATGGTCTAAATTTATGATAGATATATGATTTGGATGCTGACACCAAT 2004
Db
621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
Qy
2005 ATATTCCAAGTGGAGCAATTTGGAACGCTGAACAGGAATTCGACAGCTTAAAGACTGT 2064
Db
641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Qy
2065 TTGTGCTCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGGAGTCTGATATCCAT 2124
Db
661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Qy
2125 GTGGATGCCAACGGCATTTGATTAACGTGGAGAAATGCT 2160
Db

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RESULT 3

US-10-426-776-34

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; Sequence 34, Application US/10426776
; Publication No. US20040009553A1
; GENERAL INFORMATION:
; APPLICANT: Glucksman, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsia, Fong-Ying
; APPLICANT: Rudolf-Owen, Laura A.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.

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; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553.
; TITLE OF INVENTION: 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; TITLE OF INVENTION: 86604 AND 32222 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0620NMIM
; CURRENT APPLICATION NUMBER: US/10/426, 776
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229, 662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795, 691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185, 517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105, 992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406, 045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314, 881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773, 426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495, 823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692, 785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161, 188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 3206
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-426-776-34

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Alignment Scores:
Pred. No.: 0 Length: 3206
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

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US-10-047-855-3 (1-672) x US-10-426-776-34 (1-3206)

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Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 145 ATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACCTCTTTTACCAGGAGAAAGTTTIT 204
Qy 21 AlalleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 205 GCGATATGTGGAAGCTGTGATGCTTTGGAAACATGGAATCTCAAAATGCTGTGGCTCTT 264
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 265 CTTCCAGAGATGACACAGGTGAAGCATGCTATGAAAGCAACCATTTGTACTCAGTAGA 324
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 325 GGAGTATCAGTTTCAGTATCGCTACTTCAAAAGGGTACTTTTAAAGAACCAAGAACTATCGGT 384
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 385 GGTCCATGTCAAGTGATAGTTCACAAAGTGGGAGACTCTACTACACCAACCATCAATAACC 444

```

101 ProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
141 GluLysProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
161 LeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerProThrValLeuHis 180
181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGlu 240
241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly 300
301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360
361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysLysLeuThr 380
381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
421 ArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSer 440
441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480

1525 ATCTGCCACCAAGGATGGAATGGGATGGTAACTTATCAACATATTTTGCATGAAT 1584
481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
1585 CTGTTTGGATATAATTTTAAAACTGTTTGAATAATCTGGGAAGAGGAGATAGTG 1644
501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
1645 TTTTCTTCATTTGATGCAGATATTTGCACATGGTTTCGCAAAAGCAGAAATATCCG 1704
521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
1705 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTCGAACTCATGACCTCAGATCT 1764
541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
1765 CGGACNACCCCATTCGATGAGCTTTGACAGATTTGAAAATCTACTGGGGATAAATGTA 1824
561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
1825 CATACTGAAGACTTGTCTCAGAAACCATCTATATTCAAGAGCGCAAAAGCTAAGGACTA 1884
581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
1885 GTCATATTCTGTGGGGTGATGATACCAATGATCTCTGAAAACAGAAAGAAATTTGAAGGAA 1944
601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
1945 CTGGAGTTAATGGTCTAATTTATGATAGATATATGATGGATGCTGCAACACCAAT 2004
621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
2005 ATATTCCAGTGAGCAATTGGAACGCTGGAAGCAGAGAAATTCACAGAGCTTAAGACTGT 2064
641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
2065 TTGTGTCCCACTGTAGCCGCTTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 2124
661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
2125 GTGGATGCCACGGCATTTGATTAACGTGGAGAAATGCT 2160

RESULT 4

US-10-887-553A-1007
; Sequence 1007, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
; APPLICANT: Garza, Dan
; APPLICANT: Li, Hao
; TITLE OF INVENTION: Method to treat conditions associated
; FILE REFERENCE: 4-33262
; CURRENT APPLICATION NUMBER: US/10/887,553A
; PRIOR FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/485,883
; NUMBER OF SEQ ID NOS: 1208
; SOFTWARE: FastSeq for windows version 4.0
; SEQ ID NO 1007
; LENGTH: 3265
; TYPE: DNA
; ORGANISM: human
US-10-887-553A-1007

Alignment Scores:
Pred. No.: 0 Length: 3265
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 21

US-10-047-855-3 (1-672) x US-10-887-553A-1007 (1-3265)		QY	1	MetThrProSerGlnValAlaPheGluLeuArgGlyThrLeuLeuProGlyGluValPhe	20
QY	213	ATGACACCTTCTCAGGTGGCTTTGAAATAAGAGAACTCTTTTACCAGAGAAAGTTTTT	272		
QY	21	AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu	40		
QY	273	CGGATATGTGGAGCTGTGATGCTTTGGGAACCTGGAATCTCAAAATGCTGTGGCTCTT	332		
QY	41	LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg	60		
QY	333	CTTCAGAGAATGACACAGGTGAAGCATGTATGGAAGCAACCAATGTACTCAGTAGA	392		
QY	61	GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly	80		
QY	393	GGAGTATCAGTTCACTATCGCTACTTCAAGGGTACTTTTAGAACCCAAAGACTATCGT	452		
QY	81	GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr	100		
QY	453	GGTCCATGTCAAGTGTAGTACCAAGTGGGAGACTCATCTACAACCAACGATCAATAACC	512		
QY	101	ProLeuGluSerGluIleIleLeuAspGlyGlnPheGlyIleHisAsnGlyValGlu	120		
QY	513	CCTTTAGAAAGCGAAATTAATTATGACGATGGACAATTTGGAATCCAAATGGTGTGAA	572		
QY	121	ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer	140		
QY	573	ACTCTGGATTCTGGATGGCTGATGTCTCAGACTGAAATTAAGAAATTAACGTTTGCAATTCT	632		
QY	141	GluLysProProValSerIleThrLysLysLeuLysLysSerArgPheArgValLys	160		
QY	633	GAAAAACCTCTCTGTGTCAATACCAAGAAATAATTAATAAATCTAGATTTAGGGTGAAG	692		
QY	161	LeuThrLeuGluGlyLeuGluAspAspArgValSerProThrValLeuHis	180		
QY	693	CTGACACTAGAACCCCTGGAGGAAGATGACGATGATAGGGTATCTCCCACTGTACTCCAC	752		
QY	181	LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis	200		
QY	753	AAAATGTCCAATAGCTTGGAGATATCTTAATAAGCGACAATGAGTTCAAGTGCAGGAT	812		
QY	201	SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln	220		
QY	813	TCACGCCGAGTGTGGTATGCTTGCAGCCTGATCGTTGCAGAGAGTACAGCATACAG	872		
QY	221	ThrMetGluProAspAsnLeuGluIlePheAspPhePheGluAspLeuSerGlu	240		
QY	873	ACGATGGAACCAAGTAACTGGAACTAAATCTTTGATTTTTCGAAGAAGATCTCAGTGAG	932		
QY	241	HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer	260		
QY	933	CACGTAGTTCCAGGGTGTATGCTTCTCGGACATGTGGGTACAGCTTGTCTTATCATCC	992		
QY	261	ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn	280		
QY	993	ACCAATCTCAGAGTGGAAAGAGTGTGGAAATCTTACCTTCCCATCATGACAGCAAT	1052		
QY	281	SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly	300		
QY	1053	TCCCGGAAACAATAGGCAAGTGAGAGTTGACTATATAATTAATAAGCCATTACACGGA	1112		
QY	301	TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp	320		
QY	1113	TACAGTTGTGACATGAAATCTTCAATTTTCCAAGTATTGGAAGCCAAAGATACCATTGGAT	1172		
QY	321	ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu	340		
QY	1173	GTTGGCATCAGGTGACGAGAACTCTACAACAATCTGCCAGCTGGCTAAGTCAAGAA	1232		
QY	341	AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp	360		
QY	1233	AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCAATGTCAGCCTTTGTAGAAATTTGAC	1292		
QY	361	ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr	380		
QY	1293	GTACACCTTTCAAAGGACTTTGTGCGGTGGTATATCATGATCTTACTCTGTTGTTGACT	1352		
QY	381	MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu	400		
QY	1353	ATGAATAAGAAATTTGATGCTGATCCAGTTGAATTTATTGAAATTCAGTAAAGAAATTA	1412		
QY	401	ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp	420		
QY	1413	ACATTTGACCAATCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGGAT	1472		
QY	421	ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer	440		
QY	1473	CGGAAAGAAATCTGTGTTTCCAGGAGGAAATCTCTTTTTCAGAAATTCAGCCATTTCTTCT	1532		
QY	441	LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluLysTrp	460		
QY	1533	CTTAAGATGGTTTAGAGTCTTTGCCAAGAGATGAGGGTTTAAACATTGAAATAAATGG	1592		
QY	461	IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn	480		
QY	1593	ATCTGCCAGCAAGGATGGAATGTGGATGGTAACTTATCAACATATTTTGACATGAAT	1652		
QY	481	LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal	500		
QY	1653	CTGTTTTTGGATATAATTTTAAAAACCTGTTTAAAGAAATCTGGAAGAGGAGAAATAGTG	1712		
QY	501	PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTrpPro	520		
QY	1713	TTTTCTTTCAATTTGATGCGATATTTGCACATGGTTCCGCAAGCAGAACAAATATCCG	1772		
QY	521	IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer	540		
QY	1773	ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTCAACTCATGGACCTCAGATCT	1832		
QY	541	ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnVal	560		
QY	1833	CGGCAACCCCAATGCAATGAGCTTTGCACAGTTTGAAATCTACTGGGGATAAATGTA	1892		
QY	561	HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu	580		
QY	1893	CATACTGAGACTTGTCTCAGAACCCATCTATATTTCAAGAGGCAAAAGCTAAGGGACTA	1952		
QY	581	VallIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu	600		
QY	1953	GTCATATTTCTGCTGGGTGATGATACCAATGATCTCTGAAACAGAGGAAATTTGAAGAA	2012		
QY	601	LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn	620		
QY	2013	CTTGAGTTAATGGTCTAAATTTATGATAGGATATATGATGGATGCTTGAACCAAAAT	2072		
QY	621	IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys	640		
QY	2073	ATATTTCCAAGTGGAGCAATTTGGAAGCTGGAAGCAGGAAATTTGCCAGAGCTTAAAGAGTGT	2132		
QY	641	LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis	660		
QY	2133	TTGTGTCCTCCACTGTTAGCGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCCAT	2192		
QY	661	ValAspAlaAsnGlyIleAspAsnValGluAsnAla	672		
QY	2193	GTGGATGCCAAGCGCATTTGATAACGTGGAGAAATGCT	2228		
RESULT 5					
US-09-814-353-21000					
; Sequence 21000, Application US/09814353					
; Publication No. US20030165831A1					
; GENERAL INFORMATION:					
; APPLICANT: Lee, John					
; APPLICANT: Thompson, Pamela					
; APPLICANT: Lillie, James					

;; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;; FILE REFERENCE: MRI-006B
;; CURRENT APPLICATION NUMBER: US/09/814,353
;; CURRENT FILING DATE: 2001-03-21
;; PRIOR APPLICATION NUMBER: US 60/191,031
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: US 60/207,124
;; PRIOR FILING DATE: 2000-05-25
;; PRIOR APPLICATION NUMBER: US 60/211,940
;; PRIOR FILING DATE: 2000-06-15
;; PRIOR APPLICATION NUMBER: US 60/216,820
;; PRIOR FILING DATE: 2000-07-07
;; PRIOR APPLICATION NUMBER: US 60/220,661
;; PRIOR FILING DATE: 2000-07-25
;; PRIOR APPLICATION NUMBER: US 60/257,672
;; PRIOR FILING DATE: 2000-12-21
;; NUMBER OF SEQ ID NOS: 22037
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 21000
;; LENGTH: 3499
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
;; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-21000

Alignment Scores:

Pred. No.: 0 Length: 3499
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-047-855-3 (1-672) x US-09-814-353-21000 (1-3499)

QY 1 MetThrProSerGlnValAlaPheGluLeuArgGlyThrLeuLeuProGlyGluValPhe 20
DB 221 ATGACACCTTCTCAGGTTGCTTTTGAATGAAGGAACTCTTTTACCAGGAGAGTGT 280
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyValSerProGlnAsnAlaValAlaLeu 40
DB 281 GCGATATGTGAAGCTGTGATGCTTTGGGAACTGGAACTCTCAAAATGCTGGCTCT 340
QY 41 LeuProGlnAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
DB 341 CTTCCAGAGAATGACACAGGTGAAGCATGCTATGGAAGCAACCATTTGTAAGCTAG 400
QY 61 GlyValSerValGlnTrpArgGlyPheLeuGlyValPheLeuGluProLysThrIleGly 80
DB 401 GGAGTATCAGTTCAGTATCCTACTCTTCAAGGGTACTTTTTAGAACCAAGACTATCG 460
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
DB 461 GGTCCATGTCAGTGATAGTTTCAAGTGGAGACTCATCTACCAACCATCAATAACC 520
QY 101 ProLeuGlnSerGluIleIleLeuAspAspGlyGlnPheGlyIleHisGlnValGlu 120
DB 521 CCTTTAGAAAGCGAAATTTATTTATGACATGGACAATTTGGAATCCACATGCTGTGA 580
QY 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuGluHisTrpSer 140
DB 581 ACTCTGATTTCTGGATGGCTGACATGTACAGACTGAAATGAATAGATTTCCTTTC 640
QY 141 GluLysProProValSerIleThrLysLysLysLysLysSerArgPheArgValLys 160
DB 641 GAAACCTCTCTGTCTCATACCAAGAAATTTAAATAAATCTAGATTAGGTTGAAG 700
QY 161 LeuThrLeuGluGlyLeuGluGluAspAspArgValSerProThrValLeuHis 180

DB 701 CTGACACTAGAGGCTTGAGGAAGATGACGATAGGATATCTCCCACTGACTCCAC 760
QY 181 LysMetSerAsnSerLeuGluLeuSerLeuIleSerAspAsnGluPheLysCysArgHis 200
DB 761 AAAATGTCCTCAATAGCTTGGAGATATCTTAAATGAAGGACAAATGAGTCAAGTCAGGCAT 820
QY 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTrpSerIleGln 220
DB 821 TCACAGCCGAGTGTGTTATGCTTTCAGCCCTGATCGTTGGACAGAGTACAGATACAG 880
QY 221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPhePheGluGluLeuSerGlu 240
DB 881 ACGATGGAACCCAGATAAACCCTGGAACCTAATCTTTTGAATTTTTCGAAAGAAATCTCAGTGAG 940
QY 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
DB 941 CAGGTAGTTTCAGGCTGATGCCCTTCTCGACATGTGGGTACAGCTTGTCTTATCATCC 1000
QY 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
DB 1001 ACCATTGCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGAGCAAAAT 1060
QY 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
DB 1061 TCCCGGAAACCAATAGCAAGTGAGAGTTGACTATATAATTAATTAAGCCATTACCAGGA 1120
QY 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
DB 1121 TACAGTTGTGACATGAATCTTCATTTCCAGTATTTGGAGCCAGAGATACCATTTGAT 1180
QY 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
DB 1181 GTTGGCCATCGAGGTGCAGGAACTCTCAACAACATGCCAGCTGGCTAAAGTTCAAGAA 1240
QY 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360
DB 1241 AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCAGCCCTTTGAGAAATTTGAC 1300
QY 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
DB 1301 GTACACCTTTCAAGAGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTGTTGACT 1360
QY 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
DB 1361 ATGAAAGAAATTTGATGCTGATCCAGTTGAATTTGAATTTGAAATTCAGTAAAGAAATTA 1420
QY 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
DB 1421 ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGAAATCTAAGGAT 1480
QY 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
DB 1481 CGGAAGAATCTGTGGTTCAGGAGGAAATTCCTTTTCAGAAATCAGCCATTTCTTCT 1540
QY 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluLysTrp 460
DB 1541 CTTAAGATGGTTTATAGAGTCTTTGCCAGAAGATGTAGGGTTAAACATTGAAATATAAATGG 1600
QY 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTrpPheAspMetAsn 480
DB 1601 ATCTGCGACCAAGGAGTGAATGTGGGATGGTAACTTATCAACATATTTTTCATGAAT 1660
QY 481 LeuPheLeuAspIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
DB 1661 CTGTTTTTGGATATAATTTTAAACTGTTTTAGAAAATCTCGGAAGAGGAGAGATAGTG 1720
QY 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTrpPro 520
DB 1721 TTTTCTTCAATTTGATGACAGATATTTGCACAAATGGTTTCGCAAAAGCAGAAATAATCCG 1780
QY 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540

1781 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTGAACTCATGGACCTCAGATCT 1840
Db
541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAenLeuLeuGlyIleAenVal 560
Qy
1841 CGGCAACCCCATGTCATGAGCTTTGCAAGATTTGAAATCTACTGGGGATAAATGTA 1900
Db
561 HisThrGluAenLeuLeuArgAenProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Qy
1901 CATACTGAAGACTTCTCAGAACCCATCCCTATATTAAGAGGCCAAGAGCTTAAGGACTA 1960
Db
581 ValIlePheCysTyrGlyVasPAspThrAsnAspProGluAenArgArgLysLeuGlyGlu 600
Qy
1961 GTCATATCTCTGGGGTGATGATACCAATGATCTCTGAAACAGAGAAATTTGAAGGAA 2020
Db
601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTyrMetProGluGlnProAsn 620
Qy
2021 CTTGAGTTAATGGTCTAATTTATGATAGGATATATGATGGATGCCCTGAACCAACAAAT 2080
Db
621 IlePheGlnValGlnGlnLeuGluArgLeuLysGlnGlnLeuProGluLeuLysSerCys 640
Qy
2081 ATATTCCAAAGTGAGCAATTTGAAACGCCCTGAAGCAGGAATTCAGAGCTTAAGAGCTGT 2140
Db
641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Qy
2141 TTGTGTCACACTGTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGAGCTGATATCCAT 2200
Db
661 ValAspAlaAsnGlyIleAspAsnValGluAenAla 672
Qy
2201 GTGGATGCCAACGGCATTGATAACGTGGAGATGCT 2236
Db

RESULT 6

US-10-357-930-23730
; Sequence 23730, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23730
; LENGTH: 3499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 3490, 3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-23730

Alignment Scores:
Pred. No.: 0 Length: 3499
Score: 3537.00 Matches: 672

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-10-047-855-3 (1-672) x US-10-357-930-23730 (1-3499)
Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 221 ATGACACCTTCTCAGGTGGCTTTGAAATAAGAGGAACCTCTTTTACCAGAGAGATTTTT 280
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTyrAsnProGlnAenAlaValAlaLeu 40
Db 281 GCGATATGTGGAAGCTGTGATGCTTTGGGAACTGGAATCTCTCAAAATGCTGTGGCTCTT 340
Qy 41 LeuProGluAenAspThrGlyGluSerMetLeuTyrLysAlaThrIleValLeuSerArg 60
Db 341 CTTCCAGAGAAATGACACAGGTGAAAGCATGCTATGGAAACCAACCATTTGTACTCAGTAGA 400
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 401 GGAGTATCAGTTCAGTATCGTACTTCAAAGGGTACTTTTATAGAACCAAGACTATCGGT 460
Qy 81 GlyProCysGlnValIleValHisLysTyrGluThrHisLeuGlnProArgSerIleThr 100
Db 461 GGTCCATGTCAAGTGTAGTATTCACAGTGGGAGACTCATCTACCAACCAACCATCAATAACC 520
Qy 101 ProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 521 CCTTTAGAAACGCAATTTATTTGACGATGGACAAATTTGGAATCCCAATGGTGTGAA 580
Qy 121 ThrLeuAspSerGlyTyrLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Db 581 ACTCTGGATTTCTGGATGGCTGACATGTCAGACTGAAATAGATTACGTTTGCAATTATCT 640
Qy 141 GluLysProProValSerIleThrLysLysLysLysLysSerArgPheArgValLys 160
Db 641 GAAAAACCTCTCTGTGTCAATAACCAAGAAAAAATAAAAAAATCTAGATTTAGGGTGAAG 700
Qy 161 LeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerProThrValLeuHis 180
Db 701 CTGACACTAGAAAGCCCTGGAGGAAGATGACATGATAGGGTATCTCCACATGTACTCCAC 760
Qy 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
Db 761 AAAATGTCACATAGCTTGGAGATATCTTATAGCGACAATGAGTTCAAGTGCAGGCAT 820
Qy 201 SerGlnProGluCysGlyTyrGlyLeuGlnProArgTyrThrGluTyrSerIleGln 220
Db 821 TCACAGCCGGAGTGTGGTTATGGCTTGCAGCCTGATCGTGGACAGAGTACAGCATACAG 880
Qy 221 ThrMetGluProAspAsnLeuLeuIlePheAspPhePheGluGluAspLeuSerGlu 240
Db 881 ACGATGGAAACCAAGATAACCTGGAATACTTGTGATTTTTCGAAGAAGATCTCAGTGAG 940
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 941 CACGTAGTTTCAGGGTGATGCCCTTCTCGACATGTGGGTACAGCTGTGTCTTATCATCC 1000
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAen 280
Db 1001 ACCATTGCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGAGCAAAAT 1060
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLeuLeuProLeuGly 300
Db 1061 TCCCGGAAAAACAATAGGCAAGTGAGAGTTGACTATATAATATTATTAAGCCATTACAGGA 1120
Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTyrLysProArgIleProLeuAsp 320
Db 1121 TACAGTTGTGACATGAATCTTCATTTTCCAGATATTGGAAGCCAGAAATACCATTTGAT 1180
Qy 321 ValGlyHisArgGlyValAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340


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Db 1181 GTTGCCATCGAGTCCAGAAACTCTACAACAACCTGCCAGCTGCTAAAGTTCAAGAA 1240
Qy 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyValAlaPheValGluPheAsp 360
Db 1241 AATACATATTGCTCTTTAAGAAATGCTGTAGTATGTTGAGCCCTTTGTAGAAATTGAC 1300
Qy 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
Db 1301 GTACACCTTTCAAGAGACTTTGTGCCCGTGGTATATCATCATCTTACCTGTGTTGACT 1360
Qy 381 MetLysLysValPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
Db 1361 ATGAAAAGAAATTTGATGCTGATCAGTTGAATTAATTTGAAATTCAGTAAAGAAATTA 1420
Qy 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Db 1421 ACATTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACCTGAAATCTAAGAT 1480
Qy 421 ArgLysGluSerValValGlnGluAenSerPheSerGluAenGlnProPheProSer 440
Db 1481 CGGAAGAATCTGTGTTGAGGAGGAAATTCCTTTTCAGAAATCAGCCATTTCCCTTCT 1540
Qy 441 LeuLysMetValLeuLysLeuSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
Db 1541 CTTAAGATGGTTTAGAGTCTTTGCCAGAGATGTAGGGTTTAAACATTTGAAATAAATGG 1600
Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Db 1601 ATCTGCCAGCAAGGATGGATGGGATGGTAACTTATCAACATATTTTGCATGAT 1660
Qy 481 LeuPheLeuAspIleLeuLysThrValLeuGluAenSerGlyLysArgIleVal 500
Db 1661 CTGTTTTGGATATATTTTAAAACTGTTTTAGAAAAATCTGGGAAGAGGAGAAATAGTG 1720
Qy 501 PheSerSerPheAspAlaAspLysCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1721 TTTTCTTCATTGATGCATATTTGCACAATGGTTTCGCAAAAGCAGAAACAATATCCG 1780
Qy 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1781 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTGAACTCATGACCTCAGATCT 1840
Qy 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
Db 1841 CGGACAAACCCCATTCATGATGCTTTGCACAGTTTGAATAATCTACTGGGATATAATGTA 1900
Qy 561 HisThrGluAspLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1901 CATACTGAAGACTTGCTCAGAAACCCATCTATATTCAGAGGCAAAAGCTAAGGGACTA 1960
Qy 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1961 GTCATATCTGCTGGGGTGATGATACCAATGATCCATGATATGATGATGCTCAACCAAT 2020
Qy 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 2021 CTTGGAGTTAATGGTCTAATTTATGATAGATATATGATGATGCTCAACCAAT 2080
Qy 621 IlePheGlnValGluGlnLeuGluArgLysGlnGluLeuProGluLeuLysSerCys 640
Db 2081 ATATTCCAGTGAGCAATTTGGAACCCCTCAAGCAGCAATTTGCAGAGCTTAAGAGCTGT 2140
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2141 TTGTGTCCACCTGTAGCCGCTTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 2200
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2201 GTGGATGCCACGCCATTGATAACGTGGAGATGCT 2236
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RESULT 7

US-10-357-930-29632

; Sequence 29632, Application US/10357930

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; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29632
; LENGTH: 3499
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3490..3491, 3492, 3493, 3494, 3495, 3496, 3497, 3498, 3499
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-29632
Alignment Scores:
Pred. No.: 0 Length: 3499
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 20 Gaps: 0
US-10-047-855-3 (1-672) x US-10-357-930-29632 (1-3499)
Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 221 ATGACACCTTCTCAGGTTGCCTTTGAAATAAGAGGAACTCTTTTACAGGAGAGTTT 280
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 281 CGGATATGGGAAGCTGTGATGCTTTGGGAAATCGGAATCTCTCAAAATGCTGGGCTCT 340
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 341 CTTCCAGAGAATGACACAGGTGAAGCATGCTATGGAAAGCAACCATTTGACTCACTAGA 400
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 401 CGGATATCAGTTTCAAGTATCGCTTACTTTCAAGGGGTACTTTTTAGAACCAAGACTACGGT 460
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 461 GGTCCATGTCAAGTATAGTTTACAAAGTGGGAGACTCATCTCAACCCAGATCAATAACC 520
Qy 101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 521 CTTTAGAAAGCGAAATTTATTATTGACGATGACCAATTTGGATCCACAATGGTGTGAA 580
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
```

581 ACTCGGATTCGATGGCTGACATGTCAGACTGAAATAGATTACGTTTGCATTATCT 640
 141 GluLysProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
 641 GAAAAACCTCTGTGTCAATACCAAGAAAAATTAATAAATCTAGATTAGGGTGAAG 700
 161 LeuThrLeuGluGlyLeuGluGluAspAspArgValSerProThrValLeuHis 180
 701 CTGACACTAGAAAGGCTCGAGAGAGATGACGATGATAGGGTATCTCCACACTGTACTCCAC 760
 181 LysMetSerAsnSerLeuGluLysLeuLysSerLeuLysSerLeuLysSerLeuLys 200
 761 AAAATGTCCTAGCTCGAGATATCTTAATAAGCGCAATGATGATCAAGTGGAGCAT 820
 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTTPThrGluTyrSerIleGln 220
 821 TCACAGCCGGAGTGTGGTATGGCTTCAGCTGATCGTTGGACAGAGTACAGCATACAG 880
 221 ThrMetGluProAspAsnLeuGluLeuLysLeuLysPhePheGluGluAspLeuSerGlu 240
 881 ACGATGGAACACAGATAACCTGGAACATAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAG 940
 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
 941 CACGTAGTTTCAGGGTATGCCCTTCCTGGACATGGGTACAGCTTGTCTTATCATCC 1000
 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
 1001 ACATTCCTGAGAGTGGAAAGTGTCTGGAATCTTACTCTTCCCATCATGAGCAGAAAT 1060
 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
 1061 TCCCGGAAAAACAATAGGCAAGTGAGAGTTGACTATATAATTAATTAAGCCATTAACACGGA 1120
 301 TyrSerCysAspMetLysSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
 1121 TACAGTTGTGACATGAATCTTTCATTTTCCAAAGTATTGGAAGCCAAAGATACCATTTGAT 1180
 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
 1181 GTTGGCCATCGAGTGCAGGAACTCTACAACTGCCAGCTGCCAGTAAAGTTCAAGAA 1240
 341 AsnThrIleAlaSerLeuArgAsnAlaLysHisGlyAlaAlaPheValGluPheAsp 360
 1241 AATACTATTGCTCTTTTAAAGATGCTGTGTAGTGTGCTGAGCCCTTTGTAGAATTGAC 1300
 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
 1301 GTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTGTTGACT 1360
 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
 1361 ATGAAAGAAATTTGATGCTGATCCAGTTGAATATTGAAATTCAGTAAAGAAATTA 1420
 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
 1421 ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGCTGACTGCACTGAAATCTAAGGAT 1480
 421 ArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSer 440
 1481 CGAAAGAAATCTGTGGTTCAGGAGGAAATTCCTTTTCAGAAATACGCCATTCCTCTCT 1540
 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
 1541 CTTAAGATGGTTTTAGAGTCTTTGCCAGAGAGATGAGGGTTTAACTTGAATTAATAATGG 1600
 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrThrPheAspMetAsn 480
 1601 ATCTGCCCAAGCAAGGATGGAATGTGGATGGTAACTTATCAACATATTTTGACATGAAT 1660
 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgGlyIleVal 500
 1661 CTGTTTTTGGATATAATTTTAAAGTGTTTTTTAGAAATCTGGGAAGAGAGATAGTG 1720

QY 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
 DB 1721 TTTTCTTCATTGATGACATATTTGCACAAATGGTTTCGCAAAAGCAGAAACAAATATCGG 1780
 QY 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
 DB 1781 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTCTGAACTCATGACCTCAGATCT 1840
 QY 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
 DB 1841 CGGACAAACCCCATTCGAATGAGCTTTGCACAGTTTGAANAATCTACTGGGATATAATGTA 1900
 QY 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysLysGlyLeu 580
 DB 1901 CATACTGAAGACTTGTTCAGAAACCCCATCTATATTTCAAGAGGCAAAAGCTAAGGACTA 1960
 QY 581 ValIlePheCysTrpGlyAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
 DB 1961 GTCATATTTCTGCTGGGTGATGATACCAATGATCTCTGAAACAGAAAGAAATTAAGAGGAA 2020
 QY 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
 DB 2021 CTTGGAGTTAATGGTCTAAATTTATGATGAGATATATGATTTGGATGCTGAACACCAAT 2080
 QY 621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnLeuProGluLeuLysSerCys 640
 DB 2081 ATATTCAGTGGAGCAATTTGGAACGCTGAGCAGGAAATTCAGAGCTTAAGAGCTGT 2140
 QY 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
 DB 2141 TTGTGTCCCACTGTTAGCCGCTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 2200
 QY 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
 DB 2201 GTGGATGCCACGCGCATGATTAACGTGGAGAAATGCT 2236

RESULT 8
 US-10-426-776-39
 ; Sequence 39, Application US/10426776
 ; Publication No. US20040009553A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gluckman, Maria Alexandra
 ; APPLICANT: Williamson, Mark J.
 ; APPLICANT: Tsia, Fong-Ying
 ; APPLICANT: Rudolph-Owen, Laura A.
 ; APPLICANT: Kapeller-Libermann, Rosana
 ; APPLICANT: Meyers, Rachel E.
 ; APPLICANT: Chiang, Lillian Wei-Ming
 ; APPLICANT: Hunter, John Joseph
 ; APPLICANT: Wood, Andrew
 ; APPLICANT: Jenkins, Lorayne P.
 ; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
 ; TITLE OF INVENTION: 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13,
 ; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
 ; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
 ; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
 ; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
 ; FILE REFERENCE: 86604 AND 32222 MOLECULES AND USES THEREFOR
 ; CURRENT APPLICATION NUMBER: US/10/426,776
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: 10/229,662
 ; PRIOR FILING DATE: 2002-08-28
 ; PRIOR APPLICATION NUMBER: 09/795,691
 ; PRIOR FILING DATE: 2001-02-28
 ; PRIOR APPLICATION NUMBER: 60/185,517
 ; PRIOR FILING DATE: 2000-02-28
 ; PRIOR APPLICATION NUMBER: 10/105,992
 ; PRIOR FILING DATE: 2002-03-25
 ; PRIOR APPLICATION NUMBER: 09/406,045
 ; PRIOR FILING DATE: 1999-09-27
 ; PRIOR APPLICATION NUMBER: 10/314,881

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; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161,188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 3381
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-426-776-39

Alignment Scores:
Pred. No.: 0 Length: 3381
Score: 2965.50 Matches: 571
Percent Similarity: 90.76% Conservative: 38
Best Local Similarity: 85.10% Mismatches: 33
Query Match: 83.84% Indels: 29
DB: 17 Gaps: 6

US-10-047-855-3 (1-672) x US-10-426-776-39 (1-3381)

QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
DB 186 ATGACACCTTCTCAGGTCACTTTTGAATAAGAGGAAGTCTTTTACCGAGAGGTCTTT 245
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
DB 246 GCATGTGTGGAACTGTGTGCTTGGGAACTGGAGTCTCTCAAAATGCTGTGCTCT--- 302
QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
DB 303 CTTACTGAGATGAGACAGCGGAAAGT---GTATGGAAAGCAGTGTGTTCTTTAGTAGA 359
QY 61 GlyValSerValGlnTrpArgTrpPheLysGlyTyrPheLeuGluProLysThrIleGly 80
DB 360 GGAATGCTCGTGAAGTACCGCTACTTTCAGAGGCTGCTTTTAGAACCAAGACTATCGGT 419
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
DB 420 GGTCCATGTCAAGTCATAGTTTCAAGTGGGAGCTCACTACACCAACATCAATACACC 479
QY 101 ProLeuGluSerGluIleIleLeuAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
DB 480 CCTTTAGAAACGAAATCATTTATTGACGATGGACAATTTGGAATCCACAATGCTGTGAA 539
QY 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
DB 540 ACATCGGATCTCGATGGCTTACCTGTCAGACTGAAATTAAGACTGCGTCTGCAATTTTCT 599
QY 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
DB 600 GAGAAACCTCTCTGTTTCAATACCAAGAAAGATTTCAAAATCTAGATTAGGTTAAG 659
QY 161 LeuThrLeuGluGlyLeuGluGlu-----AspAspAspArgValSerProThrVal 178
DB 660 CTTTACACTGAGGGTCTGGAGGAAGATGATGACGACGATGATAAGGCATCTCCCACTGTT 719
QY 179 LeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCys 198
DB 720 CTTTCAAGATGTCTCAATAGCTTGGAGATATCTTAAATAGTGACAATGAGTTCAAGTGC 779
QY 199 ArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSer 218
DB 780 AGGCATCTCAGCCAGAAATGTGGGTATGGCTTACAGCTGACCGCTGGACAGATGACAGC 839
QY 219 IleGlnThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeu 238

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DB 840 ATACAGACAATGAGCCGACCAACCTTGAACCTCATCTTTGACTTTTGGAGGAATCTC 899
QY 239 SerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeu 258
DB 900 AGTGACATGTAGTCCAGGGTGTATGTTCTTCTGGACATGTGGGCAAGCATGCTCTCTG 959
QY 259 SerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProfileMetSer 278
DB 960 TCATCTACCATTGCTGAGAGTGAGAGAGCGCTGGAATCCTTACTCTTCCCATCATGAGC 1019
QY 279 ArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeu 298
DB 1020 AGAAGTTCAGAAAACTATAGCAAAAGTCAGAGTTGATTTATATCATCATCAAGCCATTA 1079
QY 299 ProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIlePro 318
DB 1080 CAGGATATATGTTGTTCTATGAGTCTTCACTTCTCCAGTATTTGGAAACCAAGATACCA 1139
QY 319 LeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysVal 338
DB 1140 CTGGATGTTGGACATCGTGTGCGAGGAACTCAACAACAACCTGCCAAGCTGGCTAAAGTA 1199
QY 339 GlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGlu 358
DB 1200 CAGGAAAAATACTATTGCTTCTTTAAGAAATGCTGCCAGCCATGCTGTCAGCATTTGTG 1259
QY 359 PheAspValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCys 378
DB 1260 TTTGATGTCACCTTTCAAGAGGACTTAGTGCTGTAGTGTATCATCATCTTCACCTGCTGT 1319
QY 379 LeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLys 398
DB 1320 TTAACCTATGAAAGGAAATATGAAGCTGATCCAGTTGAAATTTGTTGAAATCCCAAGTAA 1379
QY 399 GluLeuThrPheAspGlnLeuGlnLeuLysLeuLeuHisValThrAlaLeuLysSer 418
DB 1380 GAATTAACATTCGACCAACTCCAGTTATTGAAGCTTCTCATGTGATGTCACCTATAAAC 1439
QY 419 LysAspArgLysGluSerValGlnGluAsnSerPheSerGluAsnGlnProPhe 438
DB 1440 AAGACCCAGAAACATGTATGCTGAGGAGGAAATTCCTTTCTGAAACCAACCACTTT 1499
QY 439 ProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIle 458
DB 1500 CCTTCTCTTAAGATGCTTTTAGAGTCATTGCCAGAAAAATGTAGGATTTAATATAGAAATA 1559
QY 459 LysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAsp 478
DB 1560 AAATGGATTTGCCAACACACAGGGATGGAGTATGGGACGGCAACTTATCGACATATTTGAT 1619
QY 479 MetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArg 498
DB 1620 ATGAATGCAATTTTGGATATAATTTTAAAAACTGTTTAAAGAAATTCGCGGAAAGAGAGA 1679
QY 499 IleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLys 518
DB 1680 ATAGTATTTTCTTCACTTTCATTCAGACATCTGTACAAATGCTTCGCGCAGAAACAAACA 1739
QY 519 TyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeu 538
DB 1740 TATCCCATATATTTTGGACCCCAAGGAAAGTCTGACATTTTACCCTGAACCTCATGGACCTC 1799
QY 539 ArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluLeuLeuGlyIle 558
DB 1800 AGATCTCGACAAACCCCATTCGATGAGCTTTGACAGTTTGAATAATATTTTGGGGATA 1859
QY 559 AsnValHisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLys 578
DB 1860 AATGCCCATCTGAAGATCTCTTAGAAACCCCATCTATGCTCCCAAGAGGCAAGATAG 1919
QY 579 GlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeu 598

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Db 1920 GGATGGTCAATATCTGCTGGGGTGATGATACCAATGATCTCTGAAAAACAGAGAACTG 1979
Qy LysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGln 618
Db 1980 AAGGAATTTGGAGTAATGGTCTAATATATGATAGGTAT----- 2018
Qy 619 ProAsnIlePheGlnValGluGlnLeuGluArgLeuIysGlnGluLeu----- 634
Db 2019 -----TTGTTTTTTGTAATAAAATCTCCATGGAATTTGTTCAACAGGTAGTTTATCTA 2072
Qy 635 -----ProGluLeuIysSer-----CysLeuCys 642
Db 2073 TTTTAACTATTTTAAATATAGATAGTTAGCTTAAAGTTTATCTTGACACTGTGACCTT 2132
Qy 643 ProThrValSerArgPheValProSerSerLeu 653
Db 2133 TCCAGGTGTTGAGATATGTCAAAAGCCACTTA 2165

RESULT 9
US-10-426-776-32
; Sequence 32, Application US/10426776
; Publication NO. US2004000953A1
; GENERAL INFORMATION:
; APPLICANT: Gluckman, Maria Alexandra
; APPLICANT: Williams, Mark J.
; APPLICANT: Tsia, Fong-Ying
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553.
; TITLE OF INVENTION: 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; TITLE OF INVENTION: 86604 AND 32222 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0620NMIM
; CURRENT APPLICATION NUMBER: US/10/426, 776
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229, 662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795, 691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185, 517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105, 992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406, 045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314, 881
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 09/773, 426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495, 823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692, 785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161, 188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 2738
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-426-776-32
Alignment Scores:

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Pred. No.: 1.39e-288 Length: 2738
Score: 2552.00 Matches: 486
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.15% Indels: 0
DB: 17 Gaps: 0

US-10-047-855-3 (1-672) x US-10-426-776-32 (1-2738)

Qy 187 GluIleSerIleLeuSerAspGlnPheLeuGlyCysArgHisSerGlnProGluCysGly 206
Db 18 GAGATATCTCTAATAAGCCACAATGAGTTCAGTGCAGGCANTTCACGCGGAGTGTGGT 77
Qy 207 TyrGluLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAspAsn 226
Db 78 TATGGCTTTGACGCTGATCGTTGGACAGAGTACAGCATACAGACGATGGAACCCAGATAAC 137
Qy 227 LeuGluLeuIlePheAspPheGluGluAspLeuSerGluHisValValGlnGlyAsp 246
Db 138 CTGGAACATACTTTGATTTTTTCGAAAGAGATCTCAGTGAGCACGTAGTTCAGGGTGAT 197
Qy 247 AlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGly 266
Db 198 GCCCTTCCTGGACATGTGGGTACAGCTTGCTCTTATCATCCACCAATTGCTGAGAGTGA 257
Qy 267 LysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysThrIleGly 286
Db 258 AAGAGTCTCGAATTCCTACTCTCCATCATGACGAGAAATTCCTCGGAAACCAATAGGC 317
Qy 287 LysValArgValAspTyrIleIleLeuLysProLeuProGlyTyrSerCysAspMetLys 306
Db 318 AAGTGAGAGTTGACTATATAATTTATTAAGCCATTACAGCATACAGTTGTGACATGAA 377
Qy 307 SerSerPheSerLysTyrTrpLysProArgIleProLeuAspValGlyHisArgGlyVala 326
Db 378 TCTTCAATTTTCCAAAGTATTTGGAAGCCAAAGATACCATTTGATGTTGGCCATCGAGGTGA 437
Qy 327 GlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeu 346
Db 438 GGAACCTCTACACACTGCCAGCTGGCTAAAGTTCAAGAAATACTATTGCTTCTTTA 497
Qy 347 ArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAsp 366
Db 498 AGAAATGCTGCTAGTGTGTCAGCCTTTTGTAAGATTTGACGTACACCTTTCAAGAGAC 557
Qy 367 PheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAsp 386
Db 558 TTTGTGCCCCGGGTATATCATGATCTTACCTGTTTGTGACTATGAAAAAGAAATTTGAT 617
Qy 387 AlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGln 406
Db 618 GCTGATCCAGTTGAATTTTGAATTTCCAGTAAAAAGAAATTAACATTTGACCACTCCAG 677
Qy 407 LeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValVal 426
Db 678 TTGTTAAAGCTCACCTCATGTGACTGCATGAAATCTAAGGATCGGAAAGAAATCTGTGGT 737
Qy 427 GlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetValLeuGlu 446
Db 738 CAGGAGGAAAAATTCCTTTTCAGAAAAATCAGCCATTTCTTCTCTTAAAGATGTTTAGAG 797
Qy 447 SerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnGlnArgAsp 466
Db 798 TCTTTGCCAAGAGATGAGGGTTTAAACATTGAAATAAAAATGATCTGCGCAGCAAGGAT 857
Qy 467 GlyMetTrpAspGlyAsnLeuSerThrThrPheAspMetAsnLeuPheLeuAspIleIle 486
Db 858 GGAATGTGGATGGTAACTTATCAACATATTTTGACATGAATCTGTCTTTTGTGATATAAT 917
Qy 487 LeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPheAspAla 506
Db 918 TTAATAAACTGTTTATAGAAAAATCTCGGAAAGAGAGATAGTGTCTTCTTCAATTGATGCA 977

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QY 507 AspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrGln 526
Db 978 GATATTGACAAATGGTTCGGCAAAAGCAGAAACAAATATCCGATACATATTTTAACTCAA 1037
QY 527 GlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAla 546
Db 1038 GGAAATCTGAGATTATCTGAACTCATGGACCTCAGATCTCGGACAAACCCCATGCA 1097
QY 547 MetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeu 566
Db 1098 ATGAGCTTTGCACAGTTTGAAATCTACTGGGGATAAATGTACATACTGAAGACTTGCTC 1157
QY 567 ArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGly 586
Db 1158 AGAAACCCATCTCTATATCAAGAGGCAAAAGCTTAAGGGACTAGTCTCATATTTCTGCTGGGT 1217
QY 587 AspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAsnGlyLeu 606
Db 1218 GATGATACCAATGATCTGAAACAGAGAAATTTGAGAACTTGGAGTTAATGTCTA 1277
QY 607 IleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnIlePheGlnValGluGln 626
Db 1278 ATTTATGATAGATATATGATGGATGCCCTGAACACCAATATATTTCCAGTGGAGCAA 1337
QY 627 LeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSer 646
Db 1338 TTGGAACGCTCTGAAGCAGAAATGCCAGAGCTTAAGAGCTGTTGTGTCCTCCACTGTAGC 1397
QY 647 ArgPheValProSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIle 666
Db 1398 CGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATTCATGATGATGCCAACGGCATT 1457
QY 667 AspAsnValGluAsnAla 672
Db 1458 GATACGTCGAGATGCT 1475
RESULT 10
US-10-426-776-48
; Sequence 48, Application US/10426776
; Publication No. US20040009553A1
; GENERAL INFORMATION:
; APPLICANT: Gluckeman, Maria Alexandra
; APPLICANT: Williamson, Mark J.
; APPLICANT: Tsia, Fong-Ying
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Chiang, Lillian Wei-Ming
; APPLICANT: Hunter, John Joseph
; APPLICANT: Wood, Andrew
; APPLICANT: Jenkins, Lorayne P.
; TITLE OF INVENTION: NOVEL 27411, 23413, 22438, 23553,
; TITLE OF INVENTION: 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13,
; TITLE OF INVENTION: NARC17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11,
; TITLE OF INVENTION: NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC
; TITLE OF INVENTION: 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC
; TITLE OF INVENTION: 8B, NARC 9, NARC2A, NARC 16B, NARC 1C, NARC 1A, NARC 25,
; TITLE OF INVENTION: 86604 AND 32222 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0620NIM
; CURRENT APPLICATION NUMBER: US/10/426, 776
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 10/229,662
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/795,691
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,517
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 10/105,992
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: 09/406,045
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 10/314,881
; PRIOR FILING DATE: 2002-12-09
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; PRIOR APPLICATION NUMBER: 09/773,426
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 09/495,823
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/692,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/161,188
; PRIOR FILING DATE: 1999-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 2393
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-426-776-48
Alignment Scores:
Pred. No.: 4,73e-153 Length: 2393
Score: 1399.00 Matches: 261
Percent Similarity: 95.85% Conservative: 16
Best Local Similarity: 90.31% Mismatches: 12
Query Match: 39,55% Indels: 0
DB: 17 Gaps: 0
US-10-047-855-3 (1-672) x US-10-426-776-48 (1-2393)
QY 384 LysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAsp 403
Db 71 AAATATGAAGCTGATCCAGTGAATTTTGAATCCCAAGTAAGGAATTAACATTCGAC 130
QY 404 GlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGlu 423
Db 131 CAACCTCCAGTTATTGAAGCTTCTCATGTGACTGCACTAAAAACCAAGACCAAGAAACAA 190
QY 424 SerValValGlnGluLysSerPheSerGluAsnGlnProPheProSerLeuLysMet 443
Db 191 TGTATGGCTGAGGAGGAAATTCCTTTCTGAAAAACCAACCATTTCTCTCTTAAAGATG 250
QY 444 ValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGln 463
Db 251 GTTTTAGAGTCATTCGAGAAATGTAGGATTTAATATAGAAATAAATAGGATTCGCAA 310
QY 464 GlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeu 483
Db 311 CACAGGGATGGAGTATGGACGGCAACTTATCGACATATTTTGATATGAATGATATTTTG 370
QY 484 AspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgIleValPheSerSer 503
Db 371 GATATAATTTTAAAAACTGTTTTAGAAAAATTCGGGAGAGGAGAGATAGTATTTTCTTCA 430
QY 504 PheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPhe 523
Db 431 TTTGATGACAGATCTGTACAATGGTTCGGCAGAAACAAACAAATATCCCATATTTATT 490
QY 524 LeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThr 543
Db 491 TTGACCCCAAGGAAGTCTGACATTTACCTCTGAACCTCATGACCTCAGATCTCGGACACA 550
QY 544 ProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGlu 563
Db 551 CCCATTGCAATGAGCTTTGCACAGTTTGAAAAATATTTTGGGGATAAATGCCATCTGAA 610
QY 564 AspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePhe 583
Db 611 GATCTCCTTAGAAACCCATCTTATGTCCAAAGAGGCAAAAGATAAGGGATTTGGTCATATC 670
QY 584 CysTrpGlyAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuVal 603
Db 671 TGCTGGGGTGATGATACCAATGATCTGAAACAGAGAGAACTGAAGGAATTTGGAGTA 730
QY 604 AsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnIlePheGln 623
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731 AATGGTCTAATATATAGATAGGATATACAGTATGGATGGCTGACCAACCAATATATATCCAA 790

624 ValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLeuLysSerCysLeuCysPro 643

791 GTGAGCAACTGGAGCGCTGAAGCGAGAAATGCCAGAGCTTAAGAACTGTTTGTGTCCC 850

644 ThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHisValAspAla 663

851 ACTGTTAGCCACTTCATCTCTCTCTGATGGAGTCTTAAATCCATGATGGATGCT 910

664 AsnGlyIleAspAsnValGluAsnAla 672

911 AACGGCATTGATAATGTGGAGACGCT 937

RESULT 11

US-09-998-598-1849

; Sequence 1849, Application US/09998598

; Patent No. US20020150922A1

; GENERAL INFORMATION:

; APPLICANT: Stolk, John A.

; APPLICANT: Xu, Jiangchun

; APPLICANT: Chenault, Ruth A.

; APPLICANT: Mesgher, Madelein Joy

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.561

; CURRENT APPLICATION NUMBER: US/09/998,598

; CURRENT FILING DATE: 2001-11-16

; NUMBER OF SEQ ID NOS: 2606

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 1849

; LENGTH: 471

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-998-598-1849

Alignment Scores:

Pred. No.: 1,4e-86 Length: 471

Score: 824.00 Matches: 156

Percent Similarity: 100.00% Conservativity: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 23.30% Indels: 0

DB: 9 Gaps: 0

US-10-047-855-3 (1-672) x US-09-998-598-1849 (1-471)

QY 166 LeuGluLeuAspAspAspArgValSerProThrValLeuHisLysMetSerAsnSer 185

DB 2 CTGGAGGAAGATGACAGTGAAGGGTATCTCCCACTGTACTCCACAAATGTCCATAGC 61

QY 186 LeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnProGluCys 205

DB 62 TTGGAGATATCTTATTAAGCAGCAGTGAAGTTAAGTCAGGCATTACAGCCGAGTGT 121

QY 206 GlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAsp 225

DB 122 GGTATATGCTTCAGCGCTGATCGTTGGACAGAGTACAGCATACAGAGCATGGAACCATAG 181

QY 226 AsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGluHisValValGlnGly 245

DB 182 AACCTGGAACTAATCTTGAATTTTTTCGAAGAAGATCTCATGTGAGCAGCTAGTTCAGGT 241

QY 246 AspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSer 265

DB 242 GATGCCCTCTCCCGACATGCGGTACAGCTTGTCTCTTATCATCCACCATTTGCTGAGGT 301

QY 266 GlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysThrIle 285

DB 302 GGAAGAGTGTGGAATCTTACTCTCCCATCATGAGCAGAAATTCCTCCGAAACCAATA 361

QY 286 GlyLysValArgValAspTyrIleIleIleLysProLeuProGlyTyrSerCysAspMet 305

DB 362 GGCAGAGTGTGAGTGTGACTATATAATATTAAGACCATACCCAGGATACAGTTGTGACATG 421

306 LysSerSerPheSerLysTyrTrpLysProArgLysProLeuAspVal 321

422 AAATCTTCATTTCCAGTATTTGAAGCAAGCAATACCATTTGGATGTT 469

RESULT 12

US-09-814-353-16669

; Sequence 16669, Application US/09814353

; Publication No. US20030165831A1

; GENERAL INFORMATION:

; APPLICANT: Lee, John

; APPLICANT: Thompson, Pamela

; APPLICANT: Lillie, James

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

; FILE REFERENCE: MRI-008B

; CURRENT APPLICATION NUMBER: US/09/814,353

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: US 60/191,031

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: US 60/207,124

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: US 60/211,940

; PRIOR FILING DATE: 2000-06-15

; PRIOR APPLICATION NUMBER: US 60/216,820

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/220,661

; PRIOR FILING DATE: 2000-07-25

; PRIOR APPLICATION NUMBER: US 60/257,672

; PRIOR FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 22037

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16669

; LENGTH: 520

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-814-353-16669

Alignment Scores:

Pred. No.: 6,34e-74 Length: 520

Score: 717.00 Matches: 137

Percent Similarity: 99.28% Conservativity: 1

Best Local Similarity: 98.56% Mismatches: 0

Query Match: 20.27% Indels: 1

DB: 10 Gaps: 0

US-10-047-855-3 (1-672) x US-09-814-353-16669 (1-520)

QY 371 ValTyrHisAspLeuThrCysCysLeuThrMetLysLysPheAspAlaAspProVal 390

DB 104 GTATATCATGATCTTACTCTGTTGACTATCAAAAAGAAATTTGATCTGATCCAGTT 163

QY 391 GluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuLeuLysLeu 410

DB 164 GAATTTATTTGAATTCAGCAATTAACATTTTGAACCACTCCAGTTGTTAAAGCTC 223

QY 411 ThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValGlnGluAsn 430

DB 224 ACTCATGTGACTGCACATGAATCTAAGGATCGGAAGAAGATCTGTGGTTCAGGAGGAAAT 283

QY 431 SerPheSerGluAsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGlu 450

DB 284 TCTTTTCAGAAATCAGCCATTTCTTCTTTAAGATGTTTTAGAGTCTTTGCCAGAA 343

QY 451 AspValGlyPheAsnIleGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrpAsp 470

DB 344 GATGTAGGTTTAAATTTGAATTTGATCTGCCAGCAAGGATGGAATGTGGAT 403

QY 471 GlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAspIleIleLeuLysThrVal 490

DB 404 GGTAACCTTATCAACATATTTTGACATGAAUCTGTTTTGGATATAATTTTAAAAACCTGT 463

QY 491 LeuGluAsnSerGlyLysArgIleValPheSerSerPheAspAlaAspIleCys 509
Db 464 TTAGAAATTCGGGAAGAAGAAATAGTGGTTCTTCATTTCATGATGAGATATTGC 520
RESULT 13
US-09-796-692-8067
; Sequence 8067, Application US/09796692
; Publication NO. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8067
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (11)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (16)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (184)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (188)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (213)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (298)
; OTHER INFORMATION: n=A,T,C or G
; NAME/KEY: unsure
; LOCATION: (346)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-8067
Alignment Scores: 8.14e-72 Length: 436
Pred. No.:

Score: 698.00 Matches: 138
Percent Similarity: 94.52% Conservative: 0
Best Local Similarity: 94.52% Mismatches: 7
Query Match: 19.73% Indels: 1
DB: Gaps: 0
US-10-047-855-3 (1-672) x US-09-796-692-8067 (1-436)
QY 335 LeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAla 354
Db 1 CTGGCTAAAGNTCAANAATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGTCGA 60
QY 355 AlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTyrHisApp 374
Db 61 GCCTTTGTAGAAATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGTATATCATGAT 120
QY 375 LeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGlu 394
Db 121 CTTACCTGTGTGTGACTATGAAAGAAATTTGATGCTGTACAGTTGAAATTTTGA 180
QY 395 IleProValLysGluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThr 414
Db 181 ATTNCAGNAAGAATAAACAATTTGACCACTNCAGTTGTTAAAGCTCACTCATGTGACT 240
QY 415 AlaLeuLysSerLysAspArgLysGluSerValValGlnGluAsnSerPheSerGlu 434
Db 241 GCACCTGAAATCTAGGATCGAAAGAAATCTGTGTTTCAGGAGGAAATTCCTTTTCANAA 300
QY 435 AsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPhe 454
Db 301 AATCAGCCATTTCTCTTCTTAAGATGGTTTTAGAGTCTTTGCCANAAAGATGAGGGTTT 360
QY 455 AsnIleGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrp-AspGlyAsnLeuSe 474
Db 361 AACATTGAAATAAATGGATCTGCCAGCAAGGATGGATGTGGGATGGTACTTATC 420
QY 474 rThrTyrPheAspMet 479
Db 421 AACATATTTTGACATG 436
RESULT 14
US-10-040-862-8067
; Sequence 8067, Application US/10040862
; Publication NO. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14

;; PRIOR APPLICATION NUMBER: US 60/222,903
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: US 60/223,416
;; PRIOR FILING DATE: 2000-08-04
;; PRIOR APPLICATION NUMBER: US 60/223,378
;; PRIOR FILING DATE: 2000-08-07
;; PRIOR APPLICATION NUMBER: US 09/796,692
;; PRIOR FILING DATE: 2001-03-01
;; NUMBER OF SEQ ID NOS: 10467
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 8067
;; LENGTH: 436
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (11)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (16)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (184)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (188)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (213)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (298)
;; OTHER INFORMATION: n=A,T,C or G
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (346)
;; OTHER INFORMATION: n=A,T,C or G

US-10-040-862-8067
Alignment Scores:
Pred. No.: 8.14e-72 Length: 436
Score: 698.00 Matches: 138
Percent Similarity: 94.52% Conservative: 0
Best Local Similarity: 94.52% Mismatches: 7
Query Match: 19.73% Indels: 1
DB: 14 Gaps: 0

US-10-047-855-3 (1-672) x US-10-040-862-8067 (1-436)

QY 335 LeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaSerHisGlyAla 354
Db 1 CTGGCTAAGNCTCAANAAATACTATTGCTTCTTAAGAAATGCTGCTAGTCATGCTGCA 60
QY 355 AlaPheValGluPheAspValHisSerLysAspPheValProValValTyrHisAsp 374
Db 61 GCCTTTGTAGAAATTTGACGTACACCTTTCAAGGACTTTGTGCCCGGGTATATCATGAT 120
QY 375 LeuThrCysCysLeuThrMetLysLysPheAspAlaAspProValGluLeuPheGlu 394
Db 121 CTTACCTGTTGTTGGTACGTATGAAAAGAAATTTGATGCTGATACAGTTGAATTATTGAA 180
QY 395 IleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThr 414
Db 181 ATTNACAGNAAAGAAATTAACATTTGACCAACTNCAGTTGTTAAAGCTCACTCATGTGACT 240
QY 415 AlaLeuLysSerLysAspArgLysGluSerValValGlnGluGluAsnSerPheSerGlu 434
Db 241 GCACCTGAAATCTAAGGATCGAAGAAATCTGTGGTTCCAGGAGAAATTCCTTTTCANAA 300

QY 435 AsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPhe 454
Db 301 AATCAGCCATTTCCTTCTCTTAAGATGGTTTAGAGTCTTTGCCANAAAGATGTAGGGTTT 360
QY 455 AsnIleGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrp-AspGlyAsnLeuSe 474
Db 361 AACATTGAAATAAATGGATCTGCCAGCAAGGATGGAATGTGGGATGGTAACCTTATC 420
QY 474 rThrTyrPheAspMet 479
Db 421 AACATATTTTGACATG 436

RESULT 15

US-10-057-475B-8067
; Sequence 8067, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8067
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(436)
; OTHER INFORMATION: n = g, a, c or t
; US-10-057-475B-8067

Alignment Scores:
Pred. No.: 8.14e-72 Length: 436
Score: 698.00 Matches: 138
Percent Similarity: 94.52% Conservative: 0
Best Local Similarity: 94.52% Mismatches: 7
Query Match: 19.73% Indels: 1
DB: 17 Gaps: 0

US-10-047-855-3 (1-672) x US-10-057-475B-8067 (1-436)

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QY 335 LeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaSerHisGlyAla 354
Db |||||
1 CTGGCTAAAGNTCAANAATACTATTGCTCTTTAAGAAATGCTGCTAGTCATGGTGCA 60
QY 355 AlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTyrHisAsp 374
Db |||||
61 GCCTTTGTAGAAATTTGACGTACACCTTTCAAGGACTTTGTGCCCGTGGTATATCATGAT 120
QY 375 LeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGlu 394
Db |||||
121 CTTACCTGTTGTTGACTATGAAAAGAAATTTGATGCTGATACAGTTGAAATTATTTGAA 180
QY 395 IleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThr 414
Db |||||
181 ATTNCAGNAAAGAAATTAACATTTGACCACTNCAGTTGTTAAAGCTCACTCATGTGACT 240
QY 415 AlaLeuLysSerLysAspArgLysGluSerValValGlnGluAsnSerPheSerGlu 434
Db |||||
241 GCACTGAAATCTAAGGATCGAAAAGAAATCTGTGGTTCAGGAGGAAAAATTCCTTTTCANAA 300
QY 435 AsnGlnProPheProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPhe 454
Db |||||
301 AATCAGCCATTTCCCTTCTTAAAGATGGTTTTAGAGTCTTTGCCANAAAGATGAGGGTTT 360
QY 455 AsnIleGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrp-AspGlyAsnLeuSe 474
Db |||||
361 AACATTGAAATAAAATGGATCTGCCAGCAAAAGGATGGAATGTGGGGATGTTAACTTATC 420
QY 474 rThrTyrPheAspMet 479
Db |||||
421 AACATATTTTGACATG 436
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Job time : 1109 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 06:49:10 ; Search time 307 Seconds
(without alignments)
3581.687 Million cell updates/sec

Title: US-10-047-855-3

Perfect score: 3537

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=issued Patents NA -Qfmt=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents NA:*
- 2: /cgn2_6/ptodata/1/ina/5A COMB seq:*
- 3: /cgn2_6/ptodata/1/ina/5B COMB seq:*
- 4: /cgn2_6/ptodata/1/ina/6A COMB seq:*
- 5: /cgn2_6/ptodata/1/ina/6B COMB seq:*
- 6: /cgn2_6/ptodata/1/ina/6C COMB seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	654	18.5	2786	4	US-09-270-767-11893
C 2	516	14.6	1180	4	US-09-270-767-27552
C 3	462	13.1	2421	4	US-09-248-796A-1858
4	163	4.6	1161	4	US-09-328-352-1388
5	153	4.3	720	4	US-09-328-352-1148
6	145	4.1	14570	4	US-09-902-540-1012
7	136.5	3.9	759	4	US-09-543-681A-2048
8	131.5	3.7	1487	4	US-09-949-016-4403
9	128.5	3.7	1629	3	US-09-247-155-71
10	121.5	3.6	2682	3	US-09-105-697-9
11	126.5	3.6	1173	4	US-09-252-991A-1900
12	124	3.5	762	4	US-09-902-540-4278

Sequence 1707, Ap	124	3.5	771	3	US-09-134-001C-1707
Sequence 1212, Ap	124	3.5	26012	4	US-09-902-540-1212
Sequence 1, Appli	121.5	3.4	3393	3	US-09-104-324B-1
Sequence 1, Appli	121.5	3.4	3393	3	US-09-162-713-1
Sequence 212, App	120.5	3.4	7425	3	US-09-453-702B-212
Sequence 2792, Ap	120	3.4	957	4	US-09-107-532A-2792
Sequence 1377, Ap	119	3.4	879	4	US-09-543-681A-1377
Sequence 2289, Ap	115.5	3.3	1803	4	US-09-134-000C-2289
Sequence 498, App	115.5	3.3	2906	4	US-09-799-451-498
Sequence 305, App	115.5	3.3	7861	4	US-09-774-528-305
Sequence 259, App	114	3.2	591	4	US-09-248-796A-259
Sequence 2554, Ap	114	3.2	771	4	US-09-583-110-2554
Sequence 801, App	114	3.2	1599	4	US-09-107-433-801
Sequence 216, App	113	3.2	2651	3	US-08-961-527-216
Sequence 1448, Ap	113	3.2	2748	4	US-09-949-016-1448
Sequence 1076, Ap	113	3.2	6481	4	US-09-620-312D-1076
Sequence 705, App	112.5	3.2	3099	4	US-09-583-110-705
Sequence 4030, Ap	112.5	3.2	3442	4	US-09-710-279-4030
Sequence 565, App	112.5	3.2	5078	4	US-09-620-312D-565
Sequence 33, Appli	112	3.2	2748	3	US-09-199-290-33
Sequence 1, Appli	112	3.2	2748	4	US-09-821-616-33
Sequence 2260, Ap	112	3.2	3196	3	US-09-704-449-1
Sequence 4746, Ap	111.5	3.2	783	3	US-09-134-001C-2260
Sequence 12, Appli	111	3.1	2602	3	US-09-351-814-12
Sequence 202, App	110	3.1	744	4	US-09-107-532A-202
Sequence 1, Appli	110	3.1	2201	4	US-09-642-000-1
Sequence 638, App	110	3.1	2727	4	US-09-248-796A-638
Sequence 1, Appli	110	3.1	1830121	4	US-09-557-884-1
Sequence 1, Appli	110	3.1	1830121	4	US-09-643-990A-1
Sequence 3679, Ap	109	3.1	756	4	US-09-489-039A-3679
Sequence 3, Appli	108.5	3.1	2631	1	US-08-717-515-3
Sequence 5, Appli	108.5	3.1	3255	1	US-08-717-515-5

ALIGNMENTS

RESULT 1

US-09-270-767-11893/c
; Sequence 11893, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11893
; LENGTH: 2786
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-11893

Alignment Scores:
Pred. No.: 4, 14e-68 Length: 2786
Score: 654.00 Matches: 201
Percent Similarity: 47.17% Conservative: 124
Best Local Similarity: 29.17% Mismatches: 230
Query Match: 18.49% Indels: 135
DB: 4 Gaps: 26

US-10-047-855-3 (1-672) x US-09-270-767-11893 (1-2786)

QY	3	ProSerGlnValAlaPheGluLeuArg-----GlyThrLeuLeuProGlyGluValPhe 20
DB	2629	CCCACTCTCGGGAGTTCAATGTGGCTGGAGGTTCCTGGCCGCCGAGGAGCGACTG 2570
QY	21	AlaLeuGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
DB	2569	GGGCTTACCGCGGATGTGAAGCCCTCGCGGAGTGCGAGTGTCCAGAGATGTGGCTCTA 2510

QY 41 LeuProGluAenAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 2509 -----GAATCGCTGGACGAGCTCAACTGGCAGCCACGGTGGCCCTTCAGTCC 2462
QY 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 2461 TGCGCCACGCTGGAGTACCGC-----TACTTTGTCTACGTGGAGTCTCTCT 2414
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 2413 GCCTACAAGCAG-----ATCCGCGTGGGAACCCATTTCAAGCCCGACGCTCCCTGGGA 2360
QY 101 Pro----- 101
Db 2359 CCCTGTACGAGCTACAGTCAGCAGCGAGTTGGACGCTTTCGGTATTACGTCCGCAACTCC 2300
QY 102 -----LeuGluSerGluIleIleAsp----- 109
Db 2299 GATCTAAAGCCGACGGTGCACCGCGCTGGCTGAACCAATGAGCCATCTTCAGCTCAAG 2240
QY 110 -----AspGlyGlnPheGlyIleHisAenGlyValGluThrLeuAspSerGlyTrp 126
Db 2239 TTCATATGGCAGAAATGTTCAAGTCCACGAC-----ATCGACACTTTGAC----- 2192
QY 127 LeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGluLysProPro----- 144
Db 2191 -----CCCAGCACGTCCAGCTGAAGATTGTGCCGTGGAGAACCGCTGGCCCTG 2141
QY 145 -----ValSerIleThrLysLysLysLysLysSerArgPheArgValLysLeuThrLeu 163
Db 2140 CATGTGGAGTACTCCAAACAGAGGTACGGCAGAGCCAGCTGGAGCTGCAGCTACTTTC 2081
QY 164 GluGlyLeuGluGluAspAspArgValSerProThrValLeuHisLysMetSer 183
Db 2080 -----GGAGTGCCTACACCAAGGGGACATGTCTTCATCATCGCTGGCGTGGAG 2024
QY 184 AsnSerLeuGluLysSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro 203
Db 2023 AGGATGATGGAG-----CAGCACTTCCGCTTG 1997
QY 204 GluCysGlyTyrGlyLeuGlnProAspArgTyrThrGluTyrSerIleGlnThrMetGlu 223
Db 1996 GAGTGC-----TACAGATGTCAC----- 1976
QY 224 ProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGluHisValVal 243
Db 1975 -----GAATCTCTG----- 1967
QY 244 GlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAla 263
Db 1966 -----GGCAGTGCCACTCTGTCTACCTCGGACCTGACT 1934
QY 264 GluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer---ArgAsnSerArg 282
Db 1933 -----GGCAGCGAGGAGTGCTCCACTGCCGATTAAAGTCGGCAAGATGCAGAT 1883
QY 283 LysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGlyTyrSer 302
Db 1882 GAGACCTGGCGGCTGAGCTTCCCTATGTCCGGTGCAGCTTACCGCTACTCGCGC 1823
QY 303 CysAspMetLysSerSerPheSerLysTyrTrpLysProArgIlePro---LeuAspVal 321
Db 1822 CTAGACTTCAAGAACACTATGCTCACTACTGGCCCAAGAGCTGGCCCAACCTGGATGTG 1763
QY 322 GlyHisArgGlyAlaGlyAsnSerThrThrThrAlaGlnLeuAlaLysValGlnGluAsn 341
Db 1762 GGTCTATCGTGAATAATGGCAAGAT---TACATTCCAGACGCTCTCTCGGAAAGGAGAAC 1706
QY 342 ThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal 361
Db 1705 ACTATCGCGGTCTTCTCGGCGGCCCAATGAACATCACGACAGATCATCGATGTGATGTC 1646
QY 362 HisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThrMet 381

Db 1645 CATTGACTGCTGATGCTGTGCTGTGATTATACGATTTCCGACTCGGAACCTGCTCCG 1586
QY 382 LysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThr 401
Db 1585 CTGGCAAGCAGATACAGCCGCGCAGACGCTGGAGTACGTGCTGATCAAGACATAAAC 1526
QY 402 PheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArg 421
Db 1525 TATGACTGCTCAAAAGGCTGGCATCTTCTGTGATCGCA----- 1484
QY 422 LysGluSerValValGlnGluGluAsnSerPheSer-----GluAsnGln 436
Db 1483 -----GGCCAACTGAGGAGTATCTCCGCACACCCGAGCCAGGATGGAAACCCG 1430
QY 437 ProPheProSerLeu-LysMetValLeuGluSerLeuProGluAspValGlyPheAsn 456
Db 1429 ATATTCCCAACGCTGTGGAGGTACTGGAAAGCTGCCCAAGTCACTGGGCATTGATGT 1370
QY 456 eGluIleLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTy 476
Db 1369 GGAGATTAAAGTGG---CCACAGCGTCCGACGGC---GGAGGATCAGAGCTGAGCAAC 1316
QY 476 rPheAspMetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLy 496
Db 1315 AATCGACAAAGACTTCTTCGCCGACAGGTGATCATCAGTGTATCCAGAGGGCTGTGG 1256
QY 496 sArgArgIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysG 516
Db 1255 CAGACCCATAATCTTCTCCAGCTTCGATGCTGACATGTGCACGATGCTGAGGTTCAGCA 1196
QY 516 nAsnLysTyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMe 536
Db 1195 GAACGCTCTCCAGTGATGTTCTTCACGCGAGGAGACGAAAGAGTGGCAGCGCTTCTCT 1136
QY 536 tAspLeuArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeu 556
Db 1135 GGATCTCGAACACCGGACCTTTATTGACGCGTAAACAATGCTCAAGCTTTCGAGCTGGC 1076
QY 556 uGlyIleAsnValHisThrGluAspLeuLeu---ArgAsnProSer---TyrIleGln 574
Db 1075 TGGCACAGCTCCACACCGCCGAGGACTTCTCGGGGAAAATGCATCAGAAATGCTCGGAA 1016
QY 574 uAlaLysAlaLysGlyLeuValIlePheCysTyrPglyAspAspThrAsnAspProGluAs 594
Db 1015 AGCCAAAGATCTGGCCAAATAGTGTGATCTGGGGCGACGATTGCAACTCCAAGGAGCG 956
QY 594 nArgArgLysLeuLysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTr 614
Db 955 GGTGCAGTACTTACCCGATCGGGGCTACCGCCACGCTGCTACGATCGCATGATCTCTT 896
QY 614 pMetProGlu-----GlnProAsnIlePheGlnValGluGlnLeuGlu---ArgLeuLy 631
Db 895 CATGCGGAGGCGCAAGCGCGA-AGCCTTCTTCAAAATCACCCGACTGATGCCGAGTTCG 837
QY 631 sGlnGluLeuProGluLeuLysSer 639
Db 836 CGGCCGAGTGGCCGATCAAGAAAT 812

RESULT 2

US-09-270-767-27552/c
; Sequence 27552, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27552
; LENGTH: 1180

; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-27552

Alignment Scores:

Pred. No.: 5,04e-52 Length: 1180
Score: 516.00 Matches: 139
Percent Similarity: 51.72% Conservative: 71
Best Local Similarity: 34.24% Mismatches: 143
Query Match: 14.59% Indels: 53
DB: 4 Gaps: 12

US-10-047-855-3 (1-672) x US-09-270-767-27552 (1-1180)

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QY 216 GluTyrSerIleGlnThrMetGluProAspAsnLeuGluLeuPheAspPheGlu 235
DB 1159 GAGTACTCCAAACAGGAGTACGGCAAGAGCCAGCTGGAGCTG-----CAG 1115
QY 236 GluAspLeuSerGluHisValGlnGlnGlyAspAlaLeuProGlyHisVal-----252
DB 1114 CCTACTTTCGGAGTGCCCTACACCAAGGGGACATTTGTCTCTTTTCACATCAGCTGCGC 1055
QY 252 -----252
DB 1054 CTGGAGAGGATGATGGAGCAGCACTTCGGCTGGAGTGCTACAGATGTCCAAAGCACTC 995
QY 253 ---GlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIle 271
DB 994 CTGGCAGTGCCACTCTGTCTCCTCGACCTGACT-----GGCAGCGAGGAGTG 944
QY 272 LeuThrLeuProIleMetSer---ArgAsnSerArgLysThrIleGlyLysValArgVal 290
DB 943 CTCACCTCGCATTAAGTCGGCAAGATGCAAGATGAGATGAGCCCTGGCCAGGCTGAGGCTT 884
QY 291 AspTyrIleIleIleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSer 310
DB 883 CCTATGTCGGTGCGAGCTTACCGCTACTCGCCCTAGACTTCAAGAACCTATGCT 824
QY 311 LysTyrTrpLysProArgIlePro---LeuAspValGlyHisArgGlyAlaGlyAsnSer 329
DB 823 CACTACTGCCCCAGAGCTGGCCCAACCTGGATGGATGGTTCATCGTGGAAATGCCAAGAGT 764
QY 330 ThrThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAla 349
DB 763 ---TACATTGTCAGACCTCTCTGCGAAAGGGAGAACACTATCGCGTCTTCTCTGAGCGC 707
QY 350 AlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValPro 369
DB 706 CATGAACATCAGCAGACATGATCGAGTTGGATGTCATTTGACTGCTGATGTGCTT 647
QY 370 ValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspPro 389
DB 646 GTGATTTATCAGATTTCGAGCTGCGAATGCTCCCGCTGGCAGCAGATCAGCCGCCCA 587
QY 390 ValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLys 409
DB 586 GACCAGCTGGAGTACGTGTGATCAAAAGACATAAACTATGAGTGTCTCAAAAGGCTGCGC 527
QY 410 LeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValGlnGluGlu 429
DB 526 ATCTTCTCTGTGATCGCA-----GGCCAAGTGGAGGAGTAT 491
QY 430 AsnSerPheSer-----GluAsnGlnProPheProSerLeu-LysMetVal 444
DB 490 CCTTCGCAACACGCCAGCCAGGATGGAAACCGCATATTCCCAACGCTGGTGGAGGT 431
QY 444 lleGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnG 464
DB 430 ACTGGAGAAGCTGCCCAAGTCACTGGGCAATTGATGGAGATTAAGTGG---CCACAGCG 374
QY 464 nArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAs 484
DB 373 TCGCCAGGGGC---GGAGGATCAGAGGCTGAGCAACAAATCGCAAGAACTTCTTTCGCCGA 317
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RESULT 3

US-09-248-796A-1858
Sequence 1858, Application US/09248796A
Patent No. 6747137

GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 1858
; LENGTH: 2421
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-1858

Alignment Scores:

Pred. No.: 6.2e-45 Length: 2421
Score: 462.00 Matches: 148
Percent Similarity: 44.40% Conservative: 86
Best Local Similarity: 28.08% Mismatches: 187
Query Match: 13.06% Indels: 106
DB: 4 Gaps: 19

US-10-047-855-3 (1-672) x US-09-248-796A-1858 (1-2421)

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QY 144 ProValSerIleThrLysLysLysLysLysLysSerArgPheArgValLysLeuThrLeu 163
DB 910 CCGTGTGAATTAACAAGTCTCTTAGCTAAGAGT---TTTGCTACCGAATG-----960
QY 164 GluGlyLeuGluAspAspAspArgValSerProThrValLeuHisLysMetSer 183
DB 961 -----GATACTGCTTTATCATTTATCAATTACTTGTGCTCATAAATGACA 1005
QY 184 AnSer---LeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGln 202
DB 1006 AATAATCCAGTGAACCGCCCGTGGTGTGTGATTTTACCATTTAGAGATTTCCATGGA---1062
QY 203 ProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMet 222
DB 1063 -----AGTGCCACC 1071
```

[illegible]

```

Db      2101 GAAGCTGGTACGACCACCGATGAT-----GATTATAGACAAGTTCTTTGCAG 2148
               :::          :::          |||::|||::|||::          :
Qy      545 lIeAlaMetSerPheAlaGlnPheGluAenLeuLeuGlylYleAsnValHisThrGluAsp 564
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      2149 AATGCTGTGCAGATTTCTAAATAAATGAATTTGTTGGTGATTCTATCCAATGCATTGGCA 2208
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      565 LeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCys 584
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      2209 TTAATCAAAACACCTAGATTGGCCCAAGTTGTTAAATTCGATGGATTTGGTTGTGTACC 2268
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      585 TrpGlyAspAspThrAsnAspProGluAenArgLysLeuLysGluLeuGlyValAsn 604
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      2269 TATGGTACTGAGAACAACGACGCCGAATTCGGCTAAAATTCAAATGAGAGCTGGTGTGAT 2328
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      605 GlyLeuIleTyrAspArgIle 611
               ::|||::|||::|||::
Db      2329 GCTGTCATTGTGGTAGTGTT 2349
               ::|||::|||::|||::

RESULT 4
US-09-328-352-1388
; Sequence 1388, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETE
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1388
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1388

Alignment Scores:
Pred. No.:           3,11e-09              Length:         1161
Score:             163.00                 Matches:          86
Percent Similarity: 37.90%                Conservative:     55
Best Local Similarity: 23.12%              Mismatches:      119
Query Match:       4.61%                   Indels:          112
DB:                4                      Gaps:            16

US-10-047-855-3 (1-672) x US-09-328-352-1388 (1-1161)

Qy      311 LysfYrTrpLysProArgIleProLeuAspValGlyHisArgGlyAlaGlyAenSerThr 330
               ::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      109 GAATATCAACTTCCTTAAAAAT---CTAGTAGTAGGACACCGCGCGCTAGC----- 156
               ::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      331 ThrThrAlaGlnLeuAlaLysValGlnGluAenThrIleAlaSerLeuArgAsnAlaLa 350
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      157 -----GCITTAGCTCTGNAACATACCTTTAGCTTCATATCAAAAAGCGATT 201
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      351 SerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProval 370
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      202 GATGACGGCGCAGATTTCATTGAACCGGATCTAGTCTCTACAAAAGATGCGCTACTGGTT 261
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      371 ValTyrHisAsp-----LeuThrCysCysLeu 379
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      262 GCCCGCCCATGAAAATGGATGGTGAACAAACCAATGTAGTACCTTTAGTCAGTTTGCA 321
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      380 ThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGlu 399
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      322 GACCGTAAAAAACAAAAAATATTGATGGCTGCATTAACCTGGTTGGTTTCAACGGAAGAC 381
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      400 LeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLys 419
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      382 TTCACCTTAAAGTGAATTACAG-----CAGCTTTAAGGCCCGT 417
               |||::|||::|||::|||::|||::|||::|||::|||::|||::
Qy      420 AspArgLysGluSerValValGlnGluAenSerPheSerGluAenGlnProPhePro 433
               |||::|||::|||::|||::|||::|||::|||::|||::|||::

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Db 418 GAACGTATCTCGAGTTTCGACCGCAACACAGCTTATAATGACCTTTACCTCGTCCCA 477
QY 440 SerLeuLysMetValLeuGluSerLeuProGluAasp-----Val 452
Db 478 ACTCTAGAAACAATCATCTGAGCTTCGGAAGCTAACTATAAAAGACGGGAAATATA 537
QY 453 GlyPheAsnIleGluIleLysTrpIleCysGlnGlnArgAaspGlyMetTrpAaspGlyAsn 472
Db 538 GGTATTATATTAGACGAAACAT-----561
QY 473 LeuSerThrTyrPhe---AspMetAsnLeuPheLeu---AspIleIleLeuLysThrVal 490
Db 562 ---CCGACTTATTTAAATAATCAAAATCTGGCAATGGAAGATACCTCTCTAAAAACCTTA 618
QY 491 LeuGluAsnSerGlyLysArgIleVal-----PheSerSerPheAasp-----505
Db 619 GCCAAATATAATATACACGTGATATTGCACCTGTCTATTACAGCTCTTTTGAAGTTGAG 678
QY 506 -----506
Db 679 AATCTAAAGATTTAAAGGGAGCTTGACCTTCAATAGACGCTTAAACACGCAAAAT 738
QY 509 CysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrGlnGlyLys 528
Db 739 ATTGAGCTATAGACTCAAAACATCTCGA---CCAGCAGACTCTGAGAGCTGGTGAC 795
QY 529 SerGluIleTyrProGluLeuMetAaspLeuArgSerArgThrThrProIleAlaMetSer 548
Db 796 ACTAAACCTTATCTGATTATA-----GCCACGACCAAGGGTTAAAGAT 840
QY 549 PheAlaGlnPheGluAsnLeuLeuGly-----IleAsnValHisThr 562
Db 841 GTTGCCAAATATGCAAAATGGTGTAGGACCAAGTTAAAGTTACATACGACCTTTAATAAT 900
QY 563 GluAaspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysGlyLeuValIle 582
Db 901 GATGGCTCTTATAAACTAGTACGTTTATCTGATGCACATACGCGCTGGTTTAAAGTA 960
QY 583 PheCysTrpGlyAaspThrAsnAaspProGluAsnArg-----595
Db 961 CATCCTTAT-----ACTTCCGACCAGAAAACAACTCTTACCAGCGCGTTAAG 1011
QY 596 -----ArgLysLeuLysGluLeu-----601
Db 1012 TGCAGCCAGATAAACTGCTGAACTGTGTCCTCAACTGGTGGCTTAAAGAGTTTGAAGC 1071
QY 602 -----GlyValAsnGlyLeuIleTyrAasp 609
Db 1072 TATTCAAGCGAGGTGTTGATGCGCTTTTACCGAT 1107

RESULT 5

US-09-328-352-1148
; Sequence 1148, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1148
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1148

Alignment Scores:
Pred. No.: 2,22e-08 Length: 720
Score: 153.00 Matches: 67
Percent Similarity: 37.11% Conservative: 41
Best Local Similarity: 23.02% Mismatches: 115

Query Match: 4,33% Indels: 68
DB: 4 Gaps: 9
US-10-047-855-3 (1-672) x US-09-328-352-1148 (1-720)
QY 321 ValGlyHisArgGlyValAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 16 ATTGTGTCATCGTGGTGCACGCCGA-----GAAAGTCTCTGAA 51
QY 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAasp 360
Db 52 AATACATAGGTGGTTCAGCACATATAAAATTTAGGTATTTCGGTGTGCAATTTGAT 111
QY 361 ValHisLeuSerLysAaspPheValProValValTyrHisAaspLeuThrCysCysLeuThr 380
Db 112 ATTGCTGAGCTCAAGATCAAGAGTTGGTTCGTTATTTCATGATGATAAATTTTTCGCACG 171
QY 381 MetLysLysLysPheAaspAlaAaspProValGluLeuPheGluIleProValLysGluLeu 400
Db 172 GCA-----GGTGTCCGACCAAAATTTGTAGAGCACTCAACATTTGGCTCAAGCATTA 219
QY 401 ThrPheAaspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAasp 420
Db 220 TCATTGTGATCATCGT-----234
QY 421 ArgLysGluSerValValGlnGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
Db 235 -----CAAAATTTGGCTTAACCTGGCCAACTCTGCAACCAACCCCTACT 276
QY 441 LeuLysMetValLeuGluSerLeuProGluAaspValGlyPheAsnIleGluIleLysTrp 460
Db 277 CTTACAGATGTTTTAAATTTACTTGATAACTTTTGATCATATTGAAAGTTGAAGTTAAAGCT 336
QY 461 IleCysGlnGlnArgAaspGlyMetTrpAaspGlyAsnLeuSerThrTyrPheAaspMetAsn 480
Db 337 GFA-----AGAGATATGGCA 351
QY 481 LeuPheLeuAaspIleIleLysLysThrValLeuGluAsnSerGlyLysArgIleVal 500
Db 352 TTAGCAGAAAAAGTTAGTTCAAAAGCTTGAGACTGAGTTACAAGGTTTCGAGAGAAAGTCGTG 411
QY 501 ---PheSerSerPheAaspAlaAaspIleCysThrMetValArgGlnLysGlnAsnLysTrp 519
Db 412 ACCATCAACAAGTTTTGATCTTCAAAATTTCAACCGCTTTACGTCATATTAACTCTCAATTT 471
QY 520 ProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAaspLeuArg 539
Db 472 -----AAACGCGGATTTGATTGAACCTI-----495
QY 540 SerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGly---Ile 558
Db 496 -----CCGTTGGAGCAACGGCGATTGAACCTTGCTCATCAATATGGTGTCTGT 543
QY 559 AsnValHisThrGluAaspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLys 578
Db 544 CATATTGGCTGCGCATGATCAACTTCAACAGATGAATGAATTCATTTGCTCATCAAGCT 603
QY 579 GlyLeuValIlePheCysTrpGlyAaspThrAsnAaspProGluAsnArgIleLysLeu 598
Db 604 GGTTTGAACATTAGTGTCTGG-----ACAGTGAACGATGTAGAAAGAGCAAGAGACTA 657
QY 599 LysGluLeuGlyValAsnGlyLeuIleTyrAasp 609
Db 658 CAGGATTATGATATTTCAGGGCTTATATTACAGAT 690

RESULT 6

US-09-902-540-1012
; Sequence 1012, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.

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; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1012
; LENGTH: 14570
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1012

Alignment Scores:
Pred. No.: 3, 83e-05 Length: 14570
Score: 145.00 Matches: 112
Percent Similarity: 33.64% Conservative: 70
Best Local Similarity: 20.70% Mismatches: 173
Query Match: 4.10% Indels: 187
DB: 4 Gaps: 27

US-10-047-855-3 (1-672) x US-09-902-540-1012 (1-14570)
QY 136 ArgLeuHisTyrSerGluLysProValSerIle-----ThrLysLysLysLeu-Ly 153
Db 4941 CGCTGCAATGGACAGCGAGCGACCCCGGTATCGCTCGGATCGAAGAGAGGCGACCG 5000
QY 153 slySerArgPheArgValLysLeuThrLeuGlyLeuGluGluAspAspAspAr 173
Db 5001 CCAGGCGCGTGACG-----CAGGAGTGGACCGCG 5033
QY 173 gValSerProThrValLeuHisLysMetSerAsnSerLeuGluIleSerLeuSerAs 193
Db 5034 AGCCCTGGCTGCGTTCGCGAC-----TGCGCCAGTGGCGATTC 5072
QY 193 pAsnGluPheLysCysArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspAr 213
Db 5073 CGGAGTCCAAAGCGCGCGACCGGTATCGGTTCAGTTGGATACGGACG-GCACCCCTGG 5131
QY 213 gTrpThrGluTyrSerIleGlnThrMetGluProAspAsnLeuGluLeuPheAspPh 233
Db 5132 GTGG-----5135
QY 233 ePheGluGluAspLeuSerGluHisValValGlnGlyAspAlaLeuProGlyHisValG 253
Db 5136 -----CATGGATGCCAGCCCTGGCGGTGCCCTCCAC-----5168
QY 253 yThrAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuTh 273
Db 5169 -----GAATCTTCGTCTACCGCTTCAACCGCTAG 5197
QY 273 rLeuProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyrI 293
Db 5198 CCAGCCCCACCGCGCC-----AGTCGCTACATGGCGGC-----AT 5233
QY 293 eIleIleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTr 313
Db 5234 GGCATCTCTCCCTCCCTCC-----TTCTCCGCGCGCT 5266
QY 313 pLysProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAl 333
Db 5267 GCGGCCC-----ACGTGACATCGCCACCGCTGGGGCGCG-----5303
QY 333 aGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAAser---Hi 352
Db 5304 -----GCCGTGGCGCGGAGACACGCTGGCGGCTTCGGAGCGCGCTGAGCGCTA 5356
QY 352 sGlyAlaAlaPheValPheAspValHisLeuSerLysAspPheValProValValty 372
Db 5357 TCGCAGCGACATGTGGAGCTCGACCTCCACTCACCGGCGGGAGCTCGTGTGTC 5416
QY 372 rHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLe 392

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RESULT 7

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US-09-543-681A-2048
; Sequence 2048, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A

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5417 CCATGAC-----GCCACCTGGAGCGCTGCACGCGACGCGACGCGC-----5456
QY 392 uPheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeu---Th 411
Db 5457 -----CCTCTGGCGCGCTCAGCTGCGCGAATCTCCAGCGCTGGACGCGGCTT 5506
QY 411 rHisValThrAlaLeuLysSerLysArgLysGluSerValValGlnGluAsnSe 431
Db 5507 CCACCTCAGCGCGATGAAGCGC-----5531
QY 431 rPheSerGluAsnGlnProPhe-----ProSerLeuLysMetVa 444
Db 5532 -----ACCCTCCCATTCGGGGCCAGCGCGTGCATCCCGAGCTTCGCGAATC 5581
QY 444 lLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnG 464
Db 5582 GCTGCGCGCTTCCCC---AACCTGGCGCTCAACGTGGAGCTCAAG-----5624
QY 464 nArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAs 484
Db 5625 -----CCGGATGTCCCGGCATCGAGGA 5647
QY 484 pIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPh 504
Db 5648 CACCTTCGCCCGAGTGTTCAGAGGAAGAGCGCCCTGGAGCGGTGTGCATGGCGACG-- 5705
QY 504 eAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLe 524
Db 5706 -----GAATGGACACCGTGGCGGAGCGGTGGCGGCGCTCCCT-----5747
QY 524 uThrGlnClyLysSerGluIleTyrProGlu-----LeuMetAspLe 538
Db 5748 -----TCGCGCTGCCACTTCTACCCCGCGATGCATCGCGCGCTTCGTCATCGCCT 5800
QY 538 uArgSerArgThrThrPro-----IleAlaMetSe 548
Db 5801 GCGTGGCGGAGACACGCGCGCGAGGACCGCGCTACACCGTGTCTGCATCGCGCTCTA 5860
QY 548 rPheAlaGlnPheGluAsnLeuGlyIleAsnValHisThrGluAspLeuLeuArgAs 568
Db 5861 CTTCCGTGAGATCCGG-----CTGGTGA 5884
QY 568 nProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAs 588
Db 5885 CTCGACTTCTCTCCAGCAGTGGCGCGCGCGGCAAGTGGGTCAACGTCTGGACGGTGA 5944
QY 588 pThrAsnAspProGluAsnArgArgLysLysLysGluLeuGlyValAsnGlyLeuIleTy 608
Db 5945 T-----GACCGCGCGAGATGCACCGCTCTCGCGGAGCGTGGCGGCATCATGAC 5998
QY 608 rAspArgIleTyrAspTrpMetProGluGlnProAsnIlePhe---GlnValGluGlnLe 627
Db 5999 CGACCGG-----CCGAGCGTCTCTGAGGAGCATCATGACGCG 6034
QY 627 uGluArgLeuLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSerAr 647
Db 6035 CCCCTCGAAGCGGGATAAGCCCCGAT-----TCATGCTCGCACCAACCGCTGCGACG 6088
QY 647 g 647
Db 6089 C 6089

```


[illegible]

QY 423 uSerValGlnGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMe 443
Db 586 -----AATGATTT-----CCTGATGAAAGATCCCTAC 614
QY 443 tValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGI 463
Db 615 CCTAATGGAAGCTGTTCAGAGTGCCTAACCACTAACCTCACATC----- 660
QY 463 nGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMet----- 479
Db 661 -----TTCTTTGATGTCAAAGGCCATGC 683
QY 480 -AsnLeuPheLeuAspIleIleLeuLysThrValLeuGlu-----As 493
Db 684 ACAACAGGCTACTGAGGCTCTAAGAAATGTATATGGAATTTCTCAACTGTATAATAA 743
QY 493 nSerGlyLysArgIleValPheSerSerPhe----- 504
Db 744 TAGT-----GTGCTCTGTTCTTTTTCGCCAAGATTATCTACAAGATGAG 788
QY 505 -----AspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLe 522
Db 789 ACAACAGATCGGATGTAATAACAGCATTAACCTCACAGA-----CCTTGGAGCCTAAG 842
QY 522 uPheLeuThrGlnGlySerGluIleTyrProGluLeuMetAspLeuArgSerArgTh 542
Db 843 CCATACAGGAGATGGGAAACCA-----CGCTATGATAC 875
QY 542 rThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnValHisTh 562
Db 876 TTTCTGGAAACATTTTATATTCTGTATGATGAGCATTTTCTCGATGGAGCATGATAA 935
QY 562 r-----GluAspLeuLeuArgAs 568
Db 936 TATCTTGTGTACTGTGTGAATTTTCAGCTTTCTCTCATCGCAAGATTTTGTA---TC 992
QY 568 nProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGlyAspAs 588
Db 993 CCGGCGCTACTTGAAGAAGTGGTCAGCTAAAGAAATCCAGGTGTGTGGTGGACTGTAA 1052
QY 588 pThrAsnAspProGluAsn 594
Db 1053 TACCTTTGATGAAAGAGT 1071

RESULT 10

US-09-105-697-9
; Sequence 9, Application US/09105697
; Patent No. 6228628
; GENERAL INFORMATION:
; APPLICANT: Gelfand Ph.D., David H.
; APPLICANT: Reichert, Fred L.
; TITLE OF INVENTION: MUTANT CHIMERIC DNA POLYMERASE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Roche Molecular Systems
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08876
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/105,697
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry Ph.D., Douglas A.
; REGISTRATION NUMBER: 35321
; REFERENCE/DOCKET NUMBER: 1043

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)814-2974
; TELEFAX: (510)814-2977
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2682 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-105-697-9

Alignment Scores:

Pred. No.: 0.000203 Length: 2682
Score: 128.50 Matches: 140
Percent Similarity: 31.91% Conservative: 69
Best Local Similarity: 21.37% Mismatches: 195
Query Match: 3.63% Indels: 251
DB: 3 Gaps: 34

US-10-047-855-3 (1-672) x US-09-105-697-9 (1-2682)

QY 150 LysLysLeuLysLysSerArgPheArgValLysLeuThrLeuGluGluLysLeuGluAsp 169
Db 379 AAGAAGCGGAAAGAGGGCTACGAGGTCCGCATC-----CTCACCCGCCGAC 426
QY 170 AspAsp-----AspArgValSerProThrValLeuHisLysMetSer 183
Db 427 AAGACCTTTTACCAGCTCTTTCGACCCGATCCAC-----GTCTTCCACCCCGAGGGG 480
QY 184 AsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnPro 203
Db 481 TACCTCATCACCCGCGCTGGCTTTGGGAAAG----- 513
QY 204 GluCysGlyTyrGlyLeuGlnProAspArgTThrGluTyrSerIleGlnThr---Met 222
Db 514 -----TAGCGCTGAGGCCCGACCGACTACCGGCGCTGACCGGCGCTGACCGGGGAC 564
QY 223 GluProAspAsnLeuGluIlePheAspPheGlu----- 235
Db 565 GAGTCCGACACATCCCCGGGTCTACTGGATCGGTGAGAAAGACTGCTGTTAGCTTCTA 624
QY 236 -----GluAspLeuSerGluHisValValGlnGlyAspAlaLeuPro 249
Db 625 GAGAAGTACAAAGACCTCGAAGACATACCTGATCATGTTCCGGA-----CTTCT 675
QY 250 GlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSerAla 269
Db 676 CAAAAGGTGAGAAAGCCCTCTTCGAGACAGAGAAACGCCATTTCTCAGCAAAAAGCTG 735
QY 270 GlyIleLeu-----ValArgValAspTyrIleIleIleLysProLeu--- 272
Db 736 GCGATTTCTGGAACAAACCTTCCCATTTGAATTAACCTGGGAAGAACTTCTTACACAGGC 795
QY 273 -----ThrLeuProIleMetSerArgAsnSerArgLysThrIleGlyLys 287
Db 796 TAGCAGACAGAGAAACTCTTACCACCTTTTGAAGAAGTCTGGAATTCGCATCCATCATGA 855
QY 288 -----ValArgValAspTyrIleIleIleLysProLeu--- 298
Db 856 GAACTTCAACTGTACGAGAGTCCGAACCCGTTGGATACAGAAATAGTGAAGACCTTAGTG 915
QY 299 -----ProGlyTyrSerCysAspMetLys 306
Db 916 GAATTTGAAAACTCATGAGAAACTGAGAGAAATCCCTTCGTTCCCATAGATCTTAG 975
QY 307 SerSer-----PheSerLysTyrTrpLysPro 315
Db 976 ACGTCTTCCCTCGATCTTTCAGCTGCGACATTGTGCGTATCTCTGTGCTTTTCAACCA 1035
QY 316 Arg-----IleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThr 331
Db 1036 AAGGAAGCGTACTACATACCACTCCAT-----CATAGAAGCGCCAGAACCTGGACGAA 1089

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QY 332 ThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSer 351
Db 1090 AAGAGGGTTCGAAAAAGCTCAAGAA-----ATTCTGGAGGAC 1128
QY 352 HisGlyAlaAlaPheVal-----GluPheAspValHisLeuSerLys 365
Db 1129 CCCGAGCAAGATCGTTGGTCAGAAATTTGAAATTCAGATTAACAAGGTGTGATGGTGAAG 1188
QY 366 AspPheValProVal---ValTyrHisAspLeuThrCysCysLeuThrMetLysLysLys 384
Db 1189 GGTGTGAACCTGTTCTCTCTTACTTCGAC-----ACGATGATAGCGCT 1233
QY 385 PheAspAlaAspProValGluLeuPheGluLeuProValLysGluLeuThrPheAspGln 404
Db 1234 TACCTCTTGGCCGCAAGAA-----AAGAAGTTTCAATCTCGAGCAT 1275
QY 405 LeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSer 424
Db 1276 CTC-----GCATTGAAATTTCTTGGATACAAATGACA 1308
QY 425 ValValGlnGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetVal 444
Db 1309 TCTTACCAGAGCTATGCTCTCTCT-----TTTCGCTGTTGGTTTCAGT 1356
QY 445 LeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnGln 464
Db 1357 TTTGCCGATGTTCTGTAGAAAAGCAGCGAAC-----TACTCTGTGAAGAT 1404
QY 465 ArgAsp-----GlyMetTrpAspLysAsnLeu 473
Db 1405 GCAGACATCACCTACAGACTTTTACAGACCTTGAGCTTAAAACTCCAGAGGACGATCTG 1464
QY 474 SerThrTyrPhe-----AspMet 479
Db 1465 GAAAAAGCTGTTTACAGATAGAAATGCCCTTGTGAACGTGCTTCACGGATGGAACGTG 1524
QY 480 Asn---LeuPheLeuAspIle---IleLeuLysThrValLeuGluAsnSerGlyLysArg 497
Db 1525 AACGGTGTGTATGTGGACACAGAGTTCTCTGAAGAACTCTCAGAGAGGTACGGAAAAAA 1584
QY 498 -----ArgIleValPheSerSerPheAspAlaAspIle 508
Db 1585 CTCGAGAACTGGCAGAGGAAATATACAGATAGCTGGAGAGCGGTTCACATAAACTCA 1644
QY 509 CysThrMetVal-----ArgGlnLysGln 516
Db 1645 CCGAAGCAGGTTTCAAGGATCCTTTTGAAGAACTCGGCATAAAACACGTTGTAACG 1704
QY 517 AsnLys-----TyrProIleLeuPheLeuThrGlnGlyLysSer 529
Db 1705 ACGAAACGGGAGACTATTCAACACGCATAGAAAGTCTCTCAGGAACTTGCCTGTAACAC 1764
QY 530 GluIleTyrProGluLeuMetAspLeuArgSer----- 540
Db 1765 GAAATCATCTCTGATTTTGAATACAGAAAGATACAGAAATGAAATCAACCTACATA 1824
QY 541 -----ArgThrThrProIleAlaMetSerPheAlaGln 551
Db 1825 GACGCTCTTCCCAAGATGTCACCCCAAGHCCGGAAGGATTCATGCTTCTTCAATCAA 1884
QY 552 PheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuArgAsn---ProSer 570
Db 1885 ACGGGAGTCCACTGGAGACTTAGCAGCAGCATCCCAATCTTCAGAACCTCCCGCAGC 1944
QY 571 TyrIleGlnGluAlaLys-----AlaLysGlyLeuValIlePheCysTrpGlyAsp 588
Db 1945 AAAAGTGAAGGGGAAAGAAATCAGGAAACCGATAGTT----- 1983
QY 589 ThrAsnAspPro----- 592
Db 1984 CCTCAGGATCCAAACTGGTGGATGTCAGTCCGCTACTCTCCAAATAGACTGAGGATC 2043
QY 593 -----GluAsnArgArgLysLeuLysGluLeuGly-----Val 603
Db 2044 CTCGCCCATCTCAGTGGTGAATCAGAAATCTTTTGGAGGCATTCGAAGAGGGCATCGACGTC 2103
QY 604 AsnGlyLeuLeuTyrAspArgIleTyrAspTrpMetProGluGln 618
Db 2104 CACACTCTAAACAGCTTCCAGAAATATTCAACGTGAACCCGGAAGAA 2148

```

RESULT 11

US-09-252-991A-1900

; Sequence 1900, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 1900

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1900

Alignment Scores:

Pred. No.: 8,45e-05 Length: 1173

Score: 126.50 Matches: 87

Percent Similarity: 36.55% Conservative: 53

Best Local Similarity: 22.72% Mismatches: 146

Query Match: 3.58% Indels: 98

DB: 4 Gaps: 17

US-10-047-855-3 (1-672) x US-09-252-991A-1900 (1-1173)

QY 244 GlnGlyAsp-----AlaLeuProGlyHisValGlyThr-----AlaCysLeuLeu 258

Db 227 CAGGCGGATACCCCGGTGTCGCTCCCGCCGACCGGCAAGCCCGGAGCGTCTGCA 286

QY 259 SerSerThrIleAlaGluSerGlyLysSerAlaGly-----IleLeu 272

Db 287 CGCTTCGCTCGCGCGGCGGCA--GGAACATCCCGCGTCCGCGCAGCGCCATCGTGGCTG 345

QY 273 ThrLeuProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTyr 292

Db 346 GGATTTACCGCGACTTCTCGGTATATTTGAAAGCGCGCGGTGTCGACACGGTTCG--- 402

QY 293 IleIleIleLysProLeuProGlyTyrSerCysAspMetLysSerSerPheSerLysTyr 312

Db 403 -----CCATCATCGCGCGCGGAAATCCCGCGCAACCTCGAACAA--- 441

QY 313 TrpLysProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrThr 332

Db 442 ---GGAGCCACAGTCACTCTCATCTATGGACATCCGCGCGGCG--- 480

QY 333 AlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHis 352

Db 481 -----AAGGGCGAAGCGCGGAAACACCTTCGCGCAGCTTCCAGCGCTCGCTGAGCAT 534

QY 353 GlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValValTyr 372

Db 535 GCGCTCAACCGTTGGCAACTGACCTGCACCTGTCGCGGCGCGGCGGCACTGATGTGATC 594

QY 373 HisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGluLeu 392

Db 595 CAGACCCGAC--- 606

QY 393 PheGluIleProValLysGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHis 412

Db 817 TAAGTTAAAGGAAGATTATGAAAAATCCACACCTTGAACAGAATACAGAGGAAT 876
Qy 248 uProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGlyLysSe 268
Db 877 AAATGACAAGAAAGACAGGTATCACTACTATTGATCCAAATCACTGAGAAAGAAATAA 936
Qy 268 rAlaGlyIleLeuThrLeu 274
Db 937 AATGAAAGATTAAACATTTCTGTAGAGGAATCCAGAGATAAAGTTAATCAATTAGAGGA 996
Qy 275 -----ProIleMetSerArgAsnSerArgLysThrIleGlyLysValArgValAspTy 292
Db 997 AAAGACAAAATACAGACTGAAGAACTTAAACAAATCAATTGAGAAA-----CAGCA 1047
Qy 292 rIleIleIleLysProLeuProGlyTyTrSerCysAspMetLysSerSerPheSerLysTy 312
Db 1048 TCATTGACTAAAGAACTAGAGATATTAAAGTGTCAATACAAAGAGAGTGTGAGTACTCA 1107
Qy 312 rTriLysProArgIleProLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrTh 332
Db 1108 AAAGCTTTAGAGGAAGATTACAGATAGCA-----ACAAAAACAAT 1149
Qy 332 rAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeuArgAsnAla---Alase 351
Db 1150 TTGTGAGCTAACTGAAGAAAGAAAGAACTCAATGGAAGAACTAATAAGCTAGAGCTGC 1209
Qy 351 rHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAspPheValProValVa 371
Db 1210 TCATTGGTTTGGTTTACTGAATTTGAACT----- 1240
Qy 371 rTyHisAspLeuThrCysCysLeuThrMetLysLysLysPheAspAlaAspProValGl 391
Db 1241 -----ACTGTCTGCAGCTTGGAGAAATATTATGAGAACAGAACAGCAAGAAAGTTGGA 1290
Qy 391 uLeuPheGluIleProValLysLysLeuThrPheAsp-----GlnLe 405
Db 1291 AAAAAATGAAGATCAATTTGAAAATCTTACCATTGGAGCTTCAAAAGAAATCAAGTGAGCT 1350
Qy 405 u---GlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSe 424
Db 1351 GGAAGAGATGACTAAGCTTACAAATAACAAGAGTAGAAGCTTGAAGAAATGAAAAAGT 1410
Qy 424 rValValGlnGluGluAsnSerPheSerGluAsnGlnProPheProSerLeuLysMetVa 444
Db 1411 CTGGGAGAAAAGGAACACTTTTATATGAAATAAACAAATTT----- 1453
Qy 444 lLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTriPileCysGlnGl 464
Db 1454 ---GAGAAGATTGCTGAA-----GAATTAAAGGAACAGAACAGCA 1491
Qy 464 nArgAspGlyMetTriPAspGlyAsnLeuSerThrTyPheAspMetAsnLeuPheLeuAs 484
Db 1492 ACTAATTTGCTTCTCAAGCCAGAGAGAAGAGTACATGATTTGGAAAATACAGTTAAC 1551
Qy 484 pIleIle-----LeuLysThrValle 491
Db 1552 TGCCATTACCACAAGTGACAGTATTATCAAAAGAGGTTAAAGATCTAAAACTGAGCT 1611
Qy 491 uGluAsnSerGlyLysArgArgIleValPheSerSerPheAspAlaAspIleCysThrMe 511
Db 1612 TGAAAACGAGAGCTTAAAGAAATACTGAATTTAACTTCACAC-----TGCAACAA 1659
Qy 511 tValArgGlnLysGlnAsnLysTyProIleLeuPheLeuThrGlnGlyLysSerGluI 531
Db 1660 GCATT---TCACTAGAAAACAAAGAG-----CTCACACAGAAACAAGTGTAT 1704
Qy 531 eTyProGluLeuMet-----AspLeuArgSerArgThrThrProIleAlaMe 547
Db 1705 GACCTTAGAATCAAGAATCAGCAAGAGATATTATAATAACAAAAAGCAAGAGAAAG 1764
Qy 547 tSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeuAr 567
Db 1765 GATGTTGAAAACAAATAGAAAAATCTT-----CAAGAAACAGAAACCCCAATTAAG 1812

Qy 567 gAsnPro---SerTyIle---GlnGluAlaLysAlaLysGlyLeuValIlePheCysTr 585
Db 1813 AAATGAACCTAGATAATGTGAGAGAGAGCTAAAAACAGAAAAGAGATGAAGTTAAATGTAA 1872
Qy 585 pGlyAspAspThrAsnAsp-----ProGluAsnArgArgly 597
Db 1873 ATTGGACAAGAGTGAAGAAAAATTTGTAACAATTTTAAGGAAACAAGTTGAAAAATAAAACAA 1932
Qy 597 s---LeuLysGluLeuGlyValAsnGlyLeuIleTyAspArgIleTyAspTrpMetPr 616
Db 1933 GTATATTGAAGAACTTCAGCAGGAGAAATAAGGCTTTGAAAAAAAAGGTACACGAGAAAG 1992
Qy 616 oGluGlnProAsnIlePheGlnValGlu-----GlnLeuGluArgLe 630
Db 1993 CAAGCAACTCAATGTTTATGAGATAAAGGTCAATAAATTAGAGTTAGAACTAGAAAAGTGC 2052
Qy 630 uLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSerArgPheValPr 650
Db 2053 CAAACAGAAATTTGGAGAAATCACAGAC-----ACCTATCAGAAAGAAATTTGA 2100
Qy 650 oSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIleAspAsnValGl 670
Db 2101 GGCACAAAAGATATATCAGAGAAATAATCTT-----TTGGAAGAGGTTGA 2142
Qy 670 uAsnAla 672
Db 2143 GAAGCA 2149

Search completed: July 3, 2005, 11:02:02
Job time : 352 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 06:44:29 ; Search time 950 Seconds
(without alignments)
4187.438 Million cell updates/sec

Title: US-10-047-855-3
Perfect score: 3537
Sequence: 1 MTPSQVAPEIRGTLPLGEV.....LCGESDIHVANGIDNVENA 672

Scoring table: BLASTUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DB=frame+ p2n.model -DBV=xlh
-O=/cpn2_1/USPTO.spool/US10047855/runat_01072005_155528_2208/app.query.fasta_1.839
-DB=N_Geneseq_16Dec04 -QFMT=fastp -SUFFIX=ring -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10047855 @CN 1 1 644 @runat_01072005_155528_2208 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001as:.*
5: Geneseq2001bs:.*
6: Geneseq2002as:.*
7: Geneseq2002bs:.*
8: Geneseq2003as:.*
9: Geneseq2003bs:.*
10: Geneseq2003cs:.*
11: Geneseq2003ds:.*
12: Geneseq2004as:.*
13: Geneseq2004bs:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	3537	100.0 2019 13	ADR40144 Human Nar
2	3537	100.0 3206 4	AAD06010 Human neu
3	3537	100.0 3206 8	ABS56723 Human NAR
4	3537	100.0 3206 12	ADJ57933 Human NAR
5	3537	100.0 3499 5	ABV29614 Human pro

6	3537	100.0	3499	5	ADL62788	AdL62788 Human ova
7	3537	100.0	5443	12	ADN05171	AdN05171 Antipsori
8	3537	100.0	5443	13	ADS74320	AdS74320 PRO83903
9	3509	83.8	3498	5	ABV23741	Abv23741 Human pro
10	2965.5	83.8	3381	12	ADJ57938	AdJ57938 Rat NARC
11	2829.5	80.0	2477	5	ABA09667	AbA09667 Human bon
12	2552	72.2	2738	4	AAD06007	Aad06007 Human neu
13	2552	72.2	2738	12	ADJ57931	AdJ57931 Human NAR
14	2439.5	69.0	1978	5	ABA09583	AbA09583 Human bon
15	1399	39.6	2393	12	ADJ57947	AdJ57947 Rat NARC
16	1364	38.6	1803	4	AAH14905	AaH14905 Human CDN
17	1216	34.4	1929	4	AAH44173	AaH44173 Human gly
18	1102.5	31.2	768	4	AAH07671	AaH07671 Human CDN
19	1005	28.4	2792	4	ABL05249	AbL05249 Drosophil
20	922	26.1	5439	4	ABL05248	AbL05248 Drosophil
21	824	23.3	471	6	ABV88538	Abv88538 Human col
22	717	20.3	520	5	ADL42779	AdL42779 Human ova
23	667	18.9	2392	4	ABL19961	AbL19961 Drosophil
24	667	18.9	2457	4	ABL19771	AbL19771 Drosophil
25	667	18.9	7162	4	ABL19770	AbL19770 Drosophil
26	667	18.9	9667	4	ABL19960	AbL19960 Drosophil
27	666	18.8	2299	4	ABL15151	AbL15151 Drosophil
28	666	18.8	4299	4	ABL15150	AbL15150 Drosophil
29	661	18.7	2220	4	ABL28903	AbL28903 Drosophil
30	661	18.7	4220	4	ABL28902	AbL28902 Drosophil
31	628	17.8	396	5	ADI71235	AdI71235 Human ova
32	628	17.8	396	5	ADL36395	AdL36395 Human ova
33	570	16.1	425	5	ABV35865	Abv35865 Human pro
34	570	16.1	425	5	ABV44927	Abv44927 Human pro
35	564	15.9	327	5	ABV15063	Abv15063 Human pro
36	550	15.5	2100	4	ABL24297	AbL24297 Drosophil
37	550	15.5	4100	4	ABL24296	AbL24296 Drosophil
38	482.5	13.6	3672	13	ADT47737	AdT47737 Bacterial
39	473	13.4	14598	4	AAK80690	AaK80690 Human imm
40	473	13.4	14598	4	AAK79627	AaK79627 Human imm
41	472.5	13.4	359	5	ABV05894	Abv05894 Human pro
42	442	12.5	4925	8	ADA22696	Ada22696 A. goesyp
43	440	12.4	474	4	AAK61234	AaK61234 Human imm
44	432	12.2	3799	13	ADS48391	AdS48391 Bacterial
45	430.5	12.2	2226	13	ADS60798	AdS60798 Bacterial

ALIGNMENTS

RESULT 1			
ADR40144			
ID	ADR40144	standard; cDNA; 2019 BP.	
XX	ADR40144;		
AC	ADR40144;		
DT	18-NOV-2004	(first entry)	
DE	Human Narcl16b	(64549) cDNA.	
XX	Human Narcl16b	(64549) cDNA.	
KW	haematological; cytostatic; erythroid; anaemia; erythrocytosis;		
KW	bone marrow; leukaemia; platelet; thrombocytopenia; thrombosis; B-cell;		
KW	T-cells; neutropenia; gene therapy; human; ss; gene; Narcl16b.		
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
FT	1. .2019		
FT	/*tag= a		
FT	/product= "Human Narcl16b (64549) protein"		
XX			
PN	WO2004072242-A2.		
XX			
PD	26-AUG-2004.		
XX			
PF	05-FEB-2004; 2004WO-US003417.		
XX			
PR	05-FEB-2003; 2003US-0445241P.		
PR	18-FEB-2003; 2003US-0448389P.		

PR 20-MAR-2003; 2003US-0456320P.
 PR 03-APR-2003; 2003US-0460279P.
 PR 28-APR-2003; 2003US-0465924P.
 PR 13-MAY-2003; 2003US-0470052P.
 PR 26-AUG-2003; 2003US-0498106P.
 PR 04-SEP-2003; 2003US-0500179P.
 PR 15-SEP-2003; 2003US-0502909P.
 PR 10-OCT-2003; 2003US-0510351P.
 PR 17-OCT-2003; 2003US-0512380P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 PI Kelly LM, Carroll JM, Farlow D, Healy A;
 XX
 XX WPI; 2004-625850/60.
 DR P-PSDB; ADR40145.
 XX
 XX Identifying a compound capable of treating a hematological disorder
 PT comprises combining a compound to be tested with a polypeptide related
 PT with the disorder under conditions suitable for binding of the test
 PT compound to the polypeptide.
 XX
 XX Disclosure; SEQ ID NO 25; 321pp; English.
 XX
 XX The invention relates to a novel method for identifying a compound
 CC capable of treating a haematological disorder which comprises combining a
 CC compound to be tested with a specific polypeptide under conditions
 CC suitable for binding of the test compound to the polypeptide. The method
 CC of the invention has haematological and cytostatic applications and may
 CC be useful for identifying compounds for treating a haematological
 CC disorder associated with erythroid cells e.g. anaemia and erythrocytosis,
 CC bone marrow e.g. leukaemia, platelets e.g. thrombocytopenia and
 CC thrombosis or B-cells and T-cells e.g. neutropenia. The compounds
 CC identified may be utilised during gene therapy procedures. The current
 CC sequence is that of a human haematological disorder-related cDNA of the
 CC invention.
 XX
 XX Sequence 2019 BP; 633 A; 363 C; 449 G; 574 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 0 Length: 2019
 Score: 3537.00 Matches: 672
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-047-855-3 (1-672) x ADR40144 (1-2019)

QY	1	MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe	20
DB	1	ATGACACCTTCTCAGGTTGCTTTGAAATAAGAGGAACCTTTTACCAGGAGAAGTTTTT	60
QY	21	AlaileCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu	40
DB	61	GCGATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT	120
QY	41	LeuProGlnAsnAspThrGlyGluSerMetLeuTrpIlysaIaThrIleValLeuSerArg	60
DB	121	CTTCCAGAGAAATGACACAGGTGAAGCATGCTATGGAAGCAACCACTTTGACTCAGTAGA	180
QY	61	GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProIlysthrIleGly	80
DB	181	GGAGTATCAGTTTCAGTATCGCTACTCAAGGGGTACTTTTTAGAACCAAGACTATCGGT	240
QY	81	GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr	100
DB	241	GGTCCATGTCAAGTGATAGTTTCAAGTGGGAGACTCATCTACAACCAACGATCAATAACC	300
QY	101	ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu	120
DB	301	CCTTTAGAAGCCGAATTTATTTATTTGACGTGGAACATTTGGATCCCAATGTTGTGAA	360

QY	121	ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer	140
DB	361	ACTCTGGATTCTGGATGGCTGACATGTGACACTGAAATAAGATTACGTTTGCAATTATCT	420
QY	141	GluLysProProValSerIleThrIlystLysLysLeuLysLysSerArgPheArgValLys	160
DB	421	GAATAACCTCTCTGTGTCAATAACCAAGAAAAAATAAAAAAATCTAGATTTTAGGGTGAAG	480
QY	161	LeuThrLeuGluGlyLeuGluGluAspAspAspAspValSerProThrValLeuHis	180
DB	481	CTGACACTAGAAGGCTCGGAGGAAGATGACGATGATAGGGGTATCTCCCACTGTACTCCAC	540
QY	181	LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis	200
DB	541	AAATGTCCATAGCTTGGAGATATCTTAAATAAGCGACAATCAGTTCAAGTGCAGGCAT	600
QY	201	SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln	220
DB	601	TCACAGCCGAGTGTGTTATGGCTTTCAGCCCTGATCGTTGGACAGATACAGATACAG	660
QY	221	ThrMetGluProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGlu	240
DB	661	ACGATGGAACCAATACCTGGAACTAACTTTGATTTTTCGAAGAAGATCTCAGTGAG	720
QY	241	HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer	260
DB	721	CAGTAGTTCCAGGGTGATGCCCTTCCTGGACATGTGGTACAGCTGTCTCTTATCATCC	780
QY	261	ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn	280
DB	781	ACCATGCTCAGAGTGGAAGAGTGTGGAAATTTCTTACTCTCTCCCATCATGAGCAGAAAT	840
QY	281	SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly	300
DB	841	TCCCGAANAACAATAGGCAAGTGAGAGTTGACTATATATATTAATTAAGCCATTACCA	900
QY	301	TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp	320
DB	901	TACAGTTGTGACATGAATCTTCATTTTCCAAGTATTGGAAGCCAGAAATACCATTTGGAT	960
QY	321	ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu	340
DB	961	GTTGGCCATCAGGTCGAGGAAACTCTACAACAACCTGCCAGCTGGCTAAAGTTCAAGAA	1020
QY	341	AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp	360
DB	1021	AATACTATTGCTCTTTAAAGAAATGCTGCTAGTCACTGGTGAGCCTTTGTAGATTTGAC	1080
QY	361	ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr	380
DB	1081	GTACACCTTTCAAGGACTTTTGTGCCGTGGTATATCATGATCTTACCTGTTGTTGACT	1140
QY	381	MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu	400
DB	1141	ATGAAAAAGAAATTTGATGCTGATCCAGTCCAGTTGAATTTATTGAAATTTCCAGTAAAGAAATTA	1200
QY	401	ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp	420
DB	1201	ACATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACTGCAATCTAAGGAT	1260
QY	421	ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer	440
DB	1261	CGGAAAGAAATCTGTGTTTTCAGGAGGAAATTCCTTTTCAGAAATTCAGCCATCTCTCTCT	1320
QY	441	LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp	460
DB	1321	CTTAAGATGTTTTAGAGTCTTTTGGCAGAGAATGTAGGGTTTAAACATTGAAATAAAATGG	1380
QY	461	IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn	480
DB	1381	ATCTCCAGCAAGGAGTGAATGTGGGATGTGTTAATCTTATCAACATATTTTTCACATGAAT	1440
QY	481	LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgIleVal	500

Db 1441 CTTGTTTTGGATATAATTTAAACAACTGTTTGTAGAAAATTCCTGGGAAGAGGAGAAATAGTG 1500
Qy 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1501 TTTTCTTCATTGATGCAGATATTGCACAAATGGTTGGCAAAAGCAGCAAAATATCG 1560
Qy 521 IleLeuPheLeuThrGlnGlySerGluLeuTyrProGluLeuMetAspLeuArgSer 540
Db 1561 ATACTATTTTTAACTCAAGGAAAATCTGAGATTATCTCTGAACCTCATGACCTCAGATCT 1620
Qy 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnVal 560
Db 1621 CGGACAAACCCCATTCGAATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATAAATGTA 1680
Qy 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1681 CATACTGAGAGCTTGTCTAGAAACCCATCTATATTCAGAGGCAAAAGCTAAGGACTA 1740
Qy 581 ValIlePheCysTyrPglyAspThrAspThrAsnAspProGluAsnArgLysLeuLysGlu 600
Db 1741 GTCATATCTCTGGGCTGATGATACCAATGATCTCTGAAAACAGAAAGGAAATTTGAAGGAA 1800
Qy 601 LeuGlyValAsnGlyLeuLeuTyrAspArgIleTyrAspTyrMetProGluGlnProAsn 620
Db 1801 CTTGGAGTTTAATGGTCTAATTTATGATAGATATATGATTGGATGCTCGAACCAACCAAT 1860
Qy 621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
Db 1861 ATATTCCAAGTGGAGCAATTTGAAACGCTTGAGCAGGAATTTGCCAGAGCTTAAAGACTGT 1920
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 1921 TTGTGTCCCACTGTTAGCGCTTTGTGTCTCATCTTTGTGTGGGAGTCTGATATCCAT 1980
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 1981 GTGGATGCCACGGCAATTGATAACGTGGAGATGCT 2016

RESULT 2

AD06010
ID AAD06010 standard; DNA; 3206 BP.
AC AAD06010;
XX 31-JUL-2001 (first entry)
XX Human neuronal apoptosis regulated candidate (NARC) 16B DNA.
XX Human; neuronal apoptosis regulated candidate 16B; NARC 16B; cytostatic;
KW chromosome mapping; gene therapy; antisense therapy; lung disorder;
KW central nervous system disorder; apoptosis; spleen disorder; angina;
KW tuberculosis; Goodpasture's syndrome; liver disorder; jaundice;
KW infectious disorder; brain disorder; cerebral oedema; gonorrhoea;
KW heart disorder; kidney disorder; glomerulonephritis; testes; virucide;
KW epididymis disorder; skeletal muscle disorder; pancreatic disorder;
KW diabetes; cytoprotectant; immunostimulant; tumour; antiinflammatory;
KW antimicrobial; neuroprotective; gynaecological; ds.
XX Homo sapiens.
OS
XX WO200131007-A2.
PN
XX 03-MAY-2001.
PD
XX 20-OCT-2000; 2000WO-US029132.
PF
XX 22-OCT-1999; 99US-0161188P.
PR
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX Chiang LW;
PI
XX

DR WPI; 2001-308641/32.
XX Rat brain polypeptides, nucleic acids and antibodies, useful for
PT diagnosis and treatment of central nervous system disorders and disorders
PT associated with aberrant apoptosis.
XX Claim 1; Page 148; 161pp; English.
XX The invention relates to human homologues of neuronal apoptosis regulated
CC candidate (NARC) nucleic acid molecules and proteins derived from rat
CC brain and programmed cell death libraries. The nucleic acids of the
CC invention are useful for assaying the presence of a nucleic acid molecule
CC and for chromosome mapping. They are also used in gene therapy and
CC antisense therapy. The NARC sequences are useful for treating central
CC nervous system disorders and disorders involving aberrant apoptosis, for
CC inducing an immune response and for isolating binding partners. Diseases
CC treated include spleen disorders (e.g. tuberculosis and congestive
CC splenomegaly), lung disorders (e.g. adult respiratory distress syndrome,
CC Goodpasture's syndrome and bronchial asthma), liver disorders (e.g.
CC jaundice and hepatic failure), infectious disorders (e.g. viral
CC hepatitis), brain disorders (e.g. cerebral oedema, hypertensive
CC encephalopathy and hydrocephalus), heart disorders (e.g. heart failure,
CC angina and myocardial infarction), kidney disorders (e.g. cysts and
CC glomerulonephritis), testes and epididymis disorders (e.g. gonorrhoea and
CC syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic
CC disorders (e.g. pancreatitis and diabetes). The present sequence is human
CC neuronal apoptosis regulated candidate (NARC) 16B DNA
XX
SQ Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3206
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-047-855-3 (1-672) x AAD06010 (1-3206)

Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 145 ATGACACCTTCTCAGGTGGCTTTGAAATAGAGGAACCTCTTTTACGAGGAAGTTT 204
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTyrAsnProGlnAsnAlaValAlaLeu 40
Db 205 GCGATATGTGGAAAGCTGTGATGCTTTGGAAACTGGAATCTCCTCAAAATGCTGGCTCT 264
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTyrLysAlaThrIleValLeuSerArg 60
Db 265 CTTCCAGAGAAATGACACAGGTGAAAGCATGCTATGMAAGCAACCATTTGACTCAGTAGA 324
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 325 GGAGTATCAGTTTCTGATGCTGCTTCAAGAGGCTACTTTTGAACCAAGACTATCGGT 384
Qy 81 GlyProCysGlnValIleValHisLysTyrGluThrHisLeuGlnProArgSerIleThr 100
Db 385 GGTCCATGTCAAGTATAGTTCACAGTGGGAGACTCATCTACACCAACCATCAATACC 444
Qy 101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisGlnValGlu 120
Db 445 CCTTTAGAAAGCGAAATATTATTATGACGATGCAATTTGGAATCCACAATGGTGTGAA 504
Qy 121 ThrLeuAspSerGlyTyrLeuThrCysGlnThrGluIleArgLeuLeuHisTyrSer 140
Db 505 ACTCTGGATTCTGGATGGCTGATGTTCAGATGAAATAGATTTAGTTTGCATTATTCT 564
Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Db 565 GAAAAACCTCTCTGTGTCATAACCAAGAAAAAATTAATAAATCTAGATTGGGTGAAG 624
Qy 161 LeuThrLeuGluGlyLeuGluAspAspAspArgValSerProThrValLeuHis 180

PF 16-JAN-2002; 2002WO-US001098.
XX
PR 16-JAN-2001; 2001US-0262306P.
PR 15-JAN-2002; 2002US-00047855.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Chiang LW;
XX
DR WPI; 2003-058503/05.
XX P-PSDB; ABB84606.
DR
XX
XX Novel isolated programmed cell death-related polypeptide, NARC10 and
PT NARC16, useful for treating disorders associated with abnormal apoptotic
PT process e.g. Alzheimer's disease, cancer, myocardial infarction, stroke.
XX
XX
PS Claim 1; Fig 4A-C; 123pp; English.
XX
XX This invention describes novel cell death-related polypeptides NARC10 and
CC NARC16, located on chromosome 4q11-4q21 and which have cardiant, antiHIV,
CC immunosuppressive, dermatological, antiinflammatory, cerebroprotective,
CC neuroptic, neuroprotective, antianaemic, cardiant, vasotropic, antimanic,
CC antidiabetic, immunosuppressive, cytostatic; thyromimetic, nephrotropic,
CC immunostimulant, anticonvulsant, tranquiliser, hypotensive and
CC neuroleptic activity and can be used in gene therapy. The products of the
CC invention can be used to modulate NARC10 or NARC16 polypeptides or
CC polynucleotides, to map NARC genes on a chromosome, e.g. to locate gene
CC regions associated with genetic disease or to associate NARC10 or NARC16
CC with a disease. The polypeptides are also useful for modulating the
CC apoptotic process, and are therefore useful for modulating, and treating
CC disorders associated with increased apoptosis, inhibition of apoptosis or
CC disruptions in cell cycle, for regulating cellular functions including
CC programmed cell death, nucleosome assembly, phosphate homeostasis and the
CC cell cycle. Preferably, the products of the invention are useful for
CC treating disorders associated with abnormally low rate or abnormally high
CC rate of apoptosis e.g. cancers including follicular lymphomas, carcinomas
CC with p53 mutations, or hormone-dependent tumours, autoimmune disorders
CC including systemic lupus erythematosus, diabetes, graft rejection,
CC Hashimoto's thyroiditis and immune-mediated glomerulonephritis and viral
CC infections e.g. infections caused by herpes viruses, virus-induced
CC lymphocyte depletion (including acquired immunodeficiency syndrome
CC (AIDS)), neurodegenerative diseases manifested by loss of specific sets
CC of neurons (including Alzheimer's disease, Parkinson's disease,
CC amyotrophic lateral sclerosis, spinal muscular atrophy, retinitis
CC pigmentosa, and cerebellar degeneration), myelodysplastic syndromes
CC (including aplastic anaemia), ischaemic injuries (including myocardial
CC infarction, stroke and reperfusion injury), and toxin (e.g. alcohol)
CC induced liver disease, idiopathic dilated cardiomyopathy, ischaemic
CC cardiomyopathy and valvular heart disease, aplastic anaemia, chronic
CC neutropenia, and myelodysplastic syndromes, central nervous system
CC disorders, senile dementia, Huntington's disease, hypertension,
CC schizophrenia, attention deficit disorder, mania, anxiety, severe bipolar
CC affective disorder (BP-I). This sequence encodes the human NARC16 protein
CC described in the method of the invention
XX
SQ Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 3206
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-047-855-3 (1-672) x AB856723 (1-3206)

QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
DB 145 ATGACACCTTCTCAGGTTGCTTTGAAATAGAGGNACTCTTTTACCAGAGAGTTT 204
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40

Db 205 GCGATATGTGGAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT 264
QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTyrLysAlaThrIleValLeuSerArg 60
Db 265 CTTCCAGAGATGACACAGGTGAAAGCATGCTATGGAAGCAACCATCTGCTACTCAGTAGA 324
QY 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 325 GGAGTATCAGTTTCTGCTGCTTCAAGAGGTACTTTTATAGAACCAAGACTATCGGT 384
QY 81 GlyProCysGlnValIleValHisLysTyrGluThrHisLeuGlnProArgSerIleThr 100
Db 385 GTCCATGTCAAGTAGTAGTTCAAGTGGGAGACTCATCTACACCAGCATCAATPACC 444
QY 101 ProLeuGluSerGluIleIleLeuAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 445 CCTTTAGAAAGCGAAATATTATTATTCACGATGACAAATTTGGAATCCACAATGGTGTGAA 504
QY 121 ThrLeuAspSerGlyTyrPleuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Db 505 ACTCTGGATTCTGGATGGCTGACATGTGACATGTAATTAAGATTACGTTTGCATTATTCT 564
QY 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Db 565 GAAAAACCTCTGTGTGTAATACCAAGAAATAATTAATAAATCTAGATTAGGGTGAAG 624
QY 161 LeuThrLeuGluGlyLeuGluAspAspArgValSerProThrValLeuHis 180
Db 625 CTGACACTAGAGGCTGGAGGAAGATGACGATAGGGGTATCTCCCACTGACTCCAC 684
QY 181 LysMetSerAsnSerLeuGluLeuSerLeuIleSerAspAsnGluPheLysCysArgHis 200
Db 685 AAAATGTCCAATAGCTTGGAGATATCTTTAATAGCGACAATGAGTCAAGTCGAGGCAT 744
QY 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTyrTrpGluThrSerIleGln 220
Db 745 TCACAGCCGAGTGGTGTATGGCTTGCAGCTGATCGTGGACAGAGTACAGATACAG 804
QY 221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGlu 240
Db 805 ACGATGGAAACACAGATAAATCTGGAATCTTTTTCGAAGAAGATCTCAGTGAG 864
QY 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 865 CACGTAGTTTACGGTGTGATGCTTCTTGGACATGTGGGTACAGTGTCTTCTTATCATCC 924
QY 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
Db 925 ACCATTGTGAGAGTGGAAAGAGTGTGGAATCTTTACTCTTCCCATCATGAGCAAAAT 984
QY 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
Db 985 TCCCGGAAACAAATAGGCAAGTGGAGTTGACTATATAATTAATTAAGCCATTACACAGA 1044
QY 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
Db 1045 TACAGTTGTGACATGAAATCTTCAATTTCCAAAGTATTGGAAGCCCAAGAAATACCAT 1104
QY 321 ValGlyHisArgGlyValaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 1105 GTTGCCCATCGAGGTGAGGAAACCTCAACAACATGCCAGCTGGCTAAAGTTCAAGAA 1164
QY 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyValaAlaPheValGluPheAsp 360
Db 1165 AATACATTGCTTCTTTAAGAAATGCTGCTAGTCTGTCAGTGTGGTGGAGCCCTTTGAG 1224
QY 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
Db 1225 GTACACCTTTCAAGGACTTTGTGCCCGGTGATATCATGATCTTACCTGTTGTTGACT 1284
QY 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
Db 1285 ATGAAAGAAATTTGATGCTGATCCAGTTGAATTTATTTGNAATTCAGTAAAGAAATTA 1344

cerebroprotective; dermatological; virucide; neuroprotective; phosphatidylglycerolphosphate synthase; GPG synthase; human; ss.

Qy 401 ThrPheAspGlnLeuGlnLeuLeuLeuLeuLeuLeuHisValThrAlaLeuLysSerLysAsp 420
Db 1345 ACATTTGACCACTCCAGTTGTTAAAGCTCCTCATGTGACTGCCTGAAATCTAAGGAT 1404
Qy 421 ArgLysGluSerValValGlnGlnGluLysSerPheSerGluAsnGlnProPheProSer 440
Db 1405 CGGAAGAAATCTGTGTTTCAGGAGGAAATTCCTTTTCAGAAATTCAGCCATTTCTCTTCT 1464
Qy 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
Db 1465 CTTAAGATGGTTTATAGAGTCTTTCCCAAGAGATGAGGTTTAACTTGAATTAATAATGG 1524
Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTrpPheAspMetAsn 480
Db 1525 ATCTGCCAGCAAGGATGGATGTGGATGGTAACTTAACAATATTTTGACATGAAT 1584
Qy 481 LeuPheLeuAspIleLeuLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
Db 1585 CTGTTTTTGGATATAATTTTAAAACTGTTTTAGAAAATTCGGGAAAGAGAGAAATAGTG 1644
Qy 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTrpPro 520
Db 1645 TTTTCTTCATTTGATGCGAGATATTGCAATGTTTTCGCAAAATTCGGCAAAAGCAAAATATCCG 1704
Qy 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTrpProGluLeuMetAspLeuArgSer 540
Db 1705 ATACTATTTTAACTCAAGGAAATCTCAGATTTATCTGAACTCATGGACCTCAGATCT 1764
Qy 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
Db 1765 CGGCAACACCCCATTTGCAATGAGCTTTCACAGTTTGAATAATCTACTGGGATAAATGTA 1824
Qy 561 HisThrGluAspLeuArgAsnProSerTrpIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1825 CATACTGAAGACTTGCTCAGAAACCCATCCTATATTCAGAGGCAAAAGCTTAAGGACTA 1884
Qy 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1885 GTCATATTCCTGCTGGGTGATGATACCAATGATCTGAAACAGAAAGGAAATTTGAAGGAA 1944
Qy 601 LeuGlyValAsnGlyLeuIleTrpAspArgIleTrpAspTrpMetProGluLysProAsn 620
Db 1945 CTTGGAGTTAATGCTTAATTTATGATAGATATATGATGGATGCTTGGATGCTGAAACCAAT 2004
Qy 621 IlePheGlnValGlnGlnLeuGluArgLeuLysGlnGluLeuProGluLysSerCys 640
Db 2005 ATATTCCAAAGTGAGCAATTTGGAACCGCTGAAGCAGAAATTCAGAGCTTAAGAGCTGT 2064
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2065 TTGTGTCCTCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGGGGAGTCTGATATCCAT 2124
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2125 GTGGATGCCAACGCGCATTTGATAACGTGGAGATGCT 2160

RESULT 4
ADJ57933
ID ADJ57933 standard; cDNA; 3206 BP.

AC ADJ57933;

XX 06-MAY-2004 (first entry)

DT Human NARC 16B cDNA.

DE Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
KW lung disease; cirrhosis; hepatitis; atherosclerosis;
KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;
KW drug screening; gene therapy; cytostatic; hepatotropic; nootropic;

KW cerebroprotective; dermatological; virucide; neuroprotective;
KW phosphatidylglycerolphosphate synthase; GPG synthase; human; ss.
OS Homo sapiens.
XX US2004009553-A1.
XX 15-JAN-2004.
XX 30-APR-2003; 2003US-00426776.
XX 27-SEP-1999; 99US-00406045.
XX 22-OCT-1999; 99US-0161188P.
XX 31-JAN-2000; 2000US-00495823.
XX 28-FEB-2000; 2000US-0185517P.
XX 20-OCT-2000; 2000US-00692785.
XX 31-JAN-2001; 2001US-00773426.
XX 28-FEB-2001; 2001US-00795691.
XX 31-OCT-2001; 2001US-0335003P.
XX 25-MAR-2002; 2002US-00105992.
XX 28-AUG-2002; 2002US-00229662.
XX 30-OCT-2002; 2002US-00284014.
XX 30-OCT-2002; 2002US-00284059.
XX 09-DEC-2002; 2002US-00314881.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Williamson MJ, Tsai P, Rudolph-Owen LA;
XX Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
XX WPI; 2004-090469/09.
XX New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413,
XX 22438, 23553, NARC SCI or NARC I) useful for diagnosing, preventing or
XX treating disorders associated with the protein, e.g. cancer,
XX atherosclerosis or AIDS.
XX Claim 1; SEQ ID NO 34; 260pp; English.
XX The present invention provides isolated nucleic acid molecules and
XX proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SCI,
XX NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4,
XX NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20,
XX NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C,
XX NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or
XX 32222. The invention is useful in diagnosing, preventing or treating
XX disorders such as cancer, lung diseases, cirrhosis, hepatitis,
XX atherosclerosis, myocardial infarction, inflammation, anaemia,
XX glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency
XX syndrome), Parkinson's disease, Alzheimer's disease, stroke and
XX dermatitis. These may also be used in drug screening. The invention is
XX also useful in gene therapy. The present sequence is human neuronal
XX apoptosis regulated candidate (NARC) cDNA.
XX Sequence 3206 BP; 988 A; 580 C; 682 G; 956 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 0 Length: 3206
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-10-047-855-3 (1-672) x ADJ57933 (1-3206)

Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 145 ATGACACCTTCTCAGTTCGCTTTCGAATAAGAGGAACTCTTTTACCAGGAGAGTTTTT 204
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40

Db 205 GCGATATGTGGAAGCTGTGATGCTTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCTT 264
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 265 CTTCCAGAGAAATGACACAGCTGAAAGCATGCTATGGAAGCAACCACTGTACTCAGTAGA 324
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 325 GGAGTATCAGTTTCAGTATCGCTACTCTTCAAGGGTACTCTTTTAGAACCAAGACTATCGGT 384
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 385 GTTCCATGTCAGTATAGTTCACAAGTGGAGACTCATCTACACCAAGATCAATAACC 444
Qy 101 ProLeuGluSerGluIleIleLeuAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 445 CCTTTAGAAAGCGAATTTATTGACGATGGACAAFTTTGGAATCCACAATGCTGTTGAA 504
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgIleHisTyrSer 140
Db 505 ACTCTGGATTTCTGGATGGCTGACATGTCAGACTGGAATTAAGATTACGTTTGCATTAATCT 564
Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Db 565 GAAAAACCTTCCTGTGTCAATAACCAAGAAAAAATTAATAAAATCTAGATTTAGGGTGAAG 624
Qy 161 LeuThrLeuGluGlyLeuGluAspAspAspArgValSerProThrValLeuHis 180
Db 625 CTGACACTAGAGGCTCGAGGAGATGACGATGATAGGGTATCTCCACTGTACTCCAC 684
Qy 181 LysMetSerAsnSerLeuGluLeuSerLeuIleSerAspAsnGluPheLysCysArgHis 200
Db 685 AAAATGTCGAATAGCTTGGAGATATCTTAATAAGCGACAATGAGTTCAAGTCAGGCAT 744
Qy 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpGluTrpSerIleGln 220
Db 745 TCACAGCCGGAGTGTGGTATGCTGTCAGCCCTGATCGTTGGACAGAGTACAGTACAG 804
Qy 221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGlu 240
Db 805 ACGATGGAAACCATAGTAACCTGGNACTAATCTTTGATTTTTCGAAGAAGATCTCAGTGAG 864
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 865 CACGTAGTTTCAGGGTATGATGCTTCTGACATGCTGGTACAGCTTGTCTTATCATCC 924
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrIleuProIleMetSerArgAsn 280
Db 925 ACCATTGCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGAGCAGAAAT 984
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly 300
Db 985 TCCCGGAAACAATAGCAAGATGAGAGTTGACTATATAATTAATTAAGGCATATACAGGA 1044
Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
Db 1045 TACAGTTGTGACATGAAATCTTCAATTTTCAAGTATTGGAAGCCAAAGATACCATGGAT 1104
Qy 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 1105 GTTGGCCATCGAGGTGCAGAAACTCTACAACAACTGCCAGCTGGCTAAAGTTCAAGAA 1164
Qy 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaPheValGluPheAsp 360
Db 1165 AATACTATTGCTTCTTTAGAAATGCTGCTAGTCATGGTGCAGCCCTTTGTAGAAATTTGAC 1224
Qy 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
Db 1225 GTACACCTTTCAAGAGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTGTTGACT 1284
Qy 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
Db 1285 ATGAAAAAGAAATTTGATGCTGATCCAGTTGAATTTATTTGAAATTCAGTAAAGAAATTA 1344

Qy 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Db 1345 ACATTTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACATAAATCTAAGGAT 1404
Qy 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
Db 1405 CGGAAGAATCTGTGGTTCAGAGGAAAAATTCCTTTTCAGAAAAATCAGGCATTTCTCTCT 1464
Qy 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
Db 1465 CTTAAGATGCTTTTAGAGTCTTTTGCAGAAAGATGTAGGGTTAAACATTTGAAATAAATGG 1524
Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Db 1525 ATCTGCCAGCAAAAGGATGGAATGTGGATGGTAACCTTATCAACATATTTTGACATGAAT 1584
Qy 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgAlaIleVal 500
Db 1585 CTGTTTTTGGATATATAATTTTAAAAACTGTTTTTAGAAAAATTTCTGGGAAGAGGAGATAGTG 1644
Qy 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1645 TTTTCTTCAATTTGATGACATATTTGCACAAATGGTTCCGCAAAAGCAGCAACAATATCCG 1704
Qy 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1705 ATACTATTTTAACTCAAGGAAAACTGAGATTTATCTCTGAACTCATGACCTCAGATCT 1764
Qy 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
Db 1765 CGGACAAACCCCATTTGCAATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATAAATGTA 1824
Qy 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1825 CATACTGAAGACTTGTCTCAGAAACCCATCTATATTTCAAGAGCAAAAAGCTAAGGACCTA 1884
Qy 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgLysLeuLysGlu 600
Db 1885 GTCATATTTCTGTGGGTGATGATACCAATGATCTCTGAAAAACAGAAAGGAAATTTGAAGGAA 1944
Qy 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 1945 CTTGAGGTTAAATGGTCTAATTTATGATAGATATATGATTGGATGCTGCAACCAACAAA 2004
Qy 621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluProGluLeuLysSerCys 640
Db 2005 ATATTCCAAAGTGGAGCAATTGGAACCCCTGAAGCAGGAATTTCCAGAGCTTAAGAGCTGT 2064
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2065 TTGTGTCCCACTGTAGCCGCTTTGTTCCTCATCTTTGTGGGGAGTCTGATATCCAT 2124
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2125 GTGGATGCCAACGGCAATTGATAACGTGGAGATGCT 2160
RESULT 5
ABV29614
ID ABV29614 standard; cDNA; 3499 BP.
XX AC ABV29614;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 29605.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN W0200160860-A2.

XX PD 23-AUG-2001.
 XX PF 20-FEB-2001; 2001WO-US005171.
 XX PR 17-FEB-2000; 2000US-0183319P.
 XX PR 16-MAR-2000; 2000US-0189862P.
 XX PR 25-MAY-2000; 2000US-0207454P.
 XX PR 09-JUN-2000; 2000US-0211314P.
 XX PR 18-JUL-2000; 2000US-0219007P.
 XX PR 13-DEC-2000; 2000US-0255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 6349; 11750pp; English.
 XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
 XX SQ Sequence 3499 BP; 1104 A; 609 C; 736 G; 1040 T; 0 U; 10 Other;

Alignment Scores:
 Pred. No.: 0 Length: 3499
 Score: 3537.00 Matches: 672
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-047-855-3 (1-672) x ABV29614 (1-3499)

QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
 DB 221 ATGACACCTTCTCAGGTGCTTGGATTTGAATTAAGAGGAACCTTTTACCAGGAGATTTT 280
 QY 21 AlaIleCysGlySerCysAspAlaLeuGlyValThrPheAsnProGlnAsnAlaValAlaLeu 40
 DB 281 GCCTATGTGGAAGCTGTGATGCTTTGGGAACTCGAAATCCTCAAAATGCTGTGGCTCTT 340
 QY 41 LeuProGlnAsnAspThrGlyGluSerMetLeuTrpIleAlaThrIleValLeuSerArg 60
 DB 341 CTTCAGAGAAATGACACAGGTGAAGCATGCTATGAAGAGCAACCAATTTACTCAGTAGA 400
 QY 61 GlyValSerValGlnTyrArgTyrPheLeysGlyTyrPheLeuGluProIlyThrIleGly 80
 DB 401 GGAGTATCAGTTCAGTATCGTACTCTCAAGGGGTACTTTTGAACCAAGACTATCGGT 460
 QY 81 GlyProCysGlnValIleValHisLysTyrGluThrHisLeuGlnProArgSerIleThr 100
 DB 461 GGTCCATGCAAGTGATAGTTCACAGTGGGAGACTCATCTACAAACCAAGCATCAATAACC 520
 QY 101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
 DB 521 CCTTTAGAAAGCGAAATTTATTTGACGATGGACAAATTTGGATCCCAATGTTGTGAA 580

QY 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
 DB 581 ACTCTGGATTCTGGATGCTGCATGTCAGACTGAATAAGATTACGTTTGCATTATTCT 640
 QY 141 GluLysProProValSerIleThrLysLysLeuLysLysSerArgPheArgValLys 160
 DB 641 GAAAAACCTCTCTGTCTCAATAACCAAGAAAAATTAATAAATCTAGATTTAGGTGAAG 700
 QY 161 LeuThrLeuGluGlyLeuGluGluAspAspArgValSerProThrValLeuHis 180
 DB 701 CTGACACTAGAAAGGCTCGAGGAAGATGCGATGATAGGGTATCTCCCACTGTATCCAC 760
 QY 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
 DB 761 AAAATGTCCATAGCTTGGAGATATCCTTAATAAGGACAATGAGTTCAAGTCAGGCAT 820
 QY 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
 DB 821 TCACAGCGGAGTGTGTTATGCTTGCAGCCTGATCGTTGGACAGAGTACAGCATACAG 880
 QY 221 ThrMetGluProAspAsnLeuGluIlePheAspPheGluGluAspLeuSerGlu 240
 DB 881 ACGATGGAACCAAGATAACCTGGAACCTTATTTGATTTTTTCAGAGAGATCTCAGTGAG 940
 QY 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
 DB 941 CAGTGTAGTTCAGGTGATGCCCTTCTGCAGCATGTGGTACAGCTTGTCTCTTATCATCC 1000
 QY 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
 DB 1001 ACCATTGCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGACAGAAAT 1060
 QY 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly 300
 DB 1061 TCCCGGAAAAACAATAGCAAGTGAGATTGACTATATAATATTATTAAGCCATTACCAGGA 1120
 QY 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
 DB 1121 TACAGTTGTGCATGAATCTTCTTCTTCCAGATTATGGAAGCAAGAAATACCATTTGGAT 1180
 QY 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
 DB 1181 GTTGCCCATCGAGTGCAGGAAACTCTACAACTCTGCCAGCTGGCTAAAGTTCAAGAA 1240
 QY 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360
 DB 1241 AATACTATTGCTCTTTAAGAAATGCTGCTGATGCTGTCAGCTTGTAGATTGAC 1300
 QY 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
 DB 1301 GTACACCTTTCAGAGGACTTTGTGCCGTGGTATATCATGATCTTACCTGTGTTGACT 1360
 QY 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
 DB 1361 ATGAAAAAGAAATTTGATGCTGATCCAGTTGAAATTTTGGAAATTCAGTAAAGAAATTA 1420
 QY 401 ThrPheAspGlnLeuGlnLeuLeuLeuLeuThrHisValThrAlaLeuLysSerLysAsp 420
 DB 1421 ACATTGTACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACATCTAAGGAT 1480
 QY 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
 DB 1481 CGGAAAGAAATCTGTGTTTCAGGAGAAATTTCTTTTCAGAAATTCAGCCATTCTTCT 1540
 QY 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluLysTrp 460
 DB 1541 CTTAAGATGTTTATAGAGTCTTTGCGAAGATGTAGGGTTTAAATTTGAATAATAAATGG 1600
 QY 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
 DB 1601 ATCTCCAGCAAGGAGTGAATGTGGATGGTAACTTATCAACATATTTTTCACATGAAT 1660
 QY 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgIleVal 500

Db 1661 CTTGTTTGGATATAATTTTAAACACTGTTTTAGAAAATTTCTGGGAAGGAGAAVAGTG 1720
QY PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1721 TTTTCTTCATTCATGACAGATATTGACAAATGGTTCCGGAAGAGCAACAATATCCG 1780
QY IleLeuPheLeuThrGlnGlnLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1781 ATACTATTTTAACTCAAGGAAAATCTGAGATTTATCTCTGAACCTCATGGACCTCAGATCT 1840
QY ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnVal 560
Db 1841 CGGACAAACCCCAATGCAATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATAAATGTA 1900
QY HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1901 CATACTGAGACTTGTCTCAGAAACCCATCTTATATTCAGAGGCAAAAGCTAAGGACTA 1960
QY ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1961 GTCATATTCCTGCTGGGGTGATGATACCAATGATCTCTGMAAACAGAGGAATTTGAAGGAA 2020
QY LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 2021 CTTGGAGTTAATGCTCTAATTTATGATAGGATATATGATTGGATGCTGGAACCAACCAAT 2080
QY IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
Db 2081 ATATTCAGAGTGAGCAATTTGGAAACGCTGAGACAGGAATTTGCAGAGCTTAAGAGCTGT 2140
QY LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2141 TTGTGTCCCACTGTAGCGCTTTGTTCCTCATCTTTGTGTGGGAGTCTGATATCCAT 2200
QY ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2201 GTGGATGCCAACGGCATTGTATAACGTTGGAGAAATGCT 2236

RESULT 6

ADL62788
ID ADL62788 standard; DNA; 3499 BP.

XX AC ADL62788;

XX DT 20-MAY-2004 (first entry)

XX XX Human ovarian cancer DNA marker #21000.

XX DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX KW Homo sapiens.

XX OS WO200170979-A2.

XX PN 27-SEP-2001.

XX PD 21-MAR-2001; 2001WO-US009126.

XX PF 21-MAR-2000; 2000US-0191031P.

XX PR 25-MAY-2000; 2000US-0207124P.

XX PR 15-JUN-2000; 2000US-0211940P.

XX PR 07-JUL-2000; 2000US-0216820P.

XX PR 25-JUL-2000; 2000US-0220651P.

XX PR 21-DEC-2000; 2000US-0257672P.

XX XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PA Lee J, Lillie J;

XX PI WPI; 2001-611502/70.

XX DR Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

XX XX

XX PT

PT cancer cells as compared to their normal non-cancerous ovarian cells are
PT used to characterize stage, grade, histological type of ovarian cancer.
XX Disclosure; SEQ ID NO 21000; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in
XX ovarian cancer cells as compared to their expression in normal (i.e. non-
XX cancerous) ovarian cells. The invention also relates to polypeptides
XX encoded by the markers, antibodies that selectively bind to the
XX polypeptides, a method of inhibiting ovarian cancer in a patient at risk
XX of developing ovarian cancer involving inhibiting expression of a gene
XX corresponding to a marker of the invention and a method of treating a
XX patient afflicted with ovarian cancer comprising providing to cells of
XX the patient an antisense oligonucleotide complementary to a marker of the
XX invention. The markers are useful for assessing if a patient is afflicted
XX with ovarian cancer, which involves comparing the level of expression of
XX a marker in a patient sample and a normal level of expression of the
XX marker in a control non-ovarian cancer sample. A difference between the
XX expression levels indicates ovarian cancer. The level of expression of a
XX marker corresponds to a secreted protein or to a transcribed
XX polynucleotide or its portion. The level of expression of the marker is
XX assessed by detecting the presence in the sample, a protein or protein
XX fragment corresponding to the marker. The presence of protein or protein
XX fragment is detected using an antibody that specifically binds with the
XX protein or protein fragment. Alternatively, the level of expression of
XX the marker is assessed by detecting the presence of a transcribed
XX polynucleotide which anneals with the marker or anneals with a portion of
XX the polynucleotide comprising the marker, under stringent conditions. The
XX marker is also used for monitoring the progression of ovarian cancer in a
XX patient which involves detecting expression of the marker in a patient
XX sample at a first point in time, repeating the method at a subsequent
XX time and comparing the level of expression. The method is carried out
XX using an ovarian tissue sample. A composition comprising a marker,
XX polypeptide or antibody of the invention is used to treat ovarian cancer.
XX This sequence represents a human ovarian cancer DNA marker of the
XX invention.

XX Sequence 3499 BP; 1104 A; 610 C; 736 G; 1039 T; 0 U; 10 Other;

Alignment Scores:

Pred. No.: 0 Length: 3499
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-047-855-3 (1-672) x ADL62788 (1-3499)

QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 221 ATGACACCTTCTCAGGTTGCCCTTTGAATAAGAGGAACTCTTTTACCAGGAGATTTT 280
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Db 281 GCCATATGTGGAAGCTGTGATGCTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCT 340
QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 341 CTTCCAGAGAATGACACAGGTGAAAGCATGCTATGGAAGCAACCACTTGTACTCAGTAGA 400
QY 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 401 GGAGTATCAGTTCAGTATCGTACTTCAAGGGGTACTTTTAGAACCAAGACTATCGGT 460
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 461 GGTCCATGTCAAGTGATAGTTCACAAGTGGGAGACTCATCTACAACCAACCAATCAAC 520
QY 101 ProLeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisGlyValGlu 120
Db 521 CCTTTAGAAAGCGAAATTTATTGACATGGGCAATTTGGAATCCACAATGTTGTTGAA 580

```
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Db 581 ACTCTGGATTCCTGGATCGCTGACATGTCAGACTGAAATAAGATTACCGTTTGCAATATCT 640
Qy 141 GluLysProValSerIleThrLysLysLysLysLysLysSerArgPheArgValLys 160
Db 641 GAAAAACCTCTGTCTCAATACCAAGAAAAAATTAATAAGCAATAGATTAGGGTGAAG 700
Qy 161 LeuThrLeuGluGluGluAspAspAspArgValSerProThrValLeuHis 180
Db 701 CTGACACTAGAAGGCTCGAGAGAGATGACGATGATAGGGTATCTCCCACTGTACTCCAC 760
Qy 181 LysMetSerAnSerLeuGluIleSerLeuLysSerAspGluPheLysCysArgHis 200
Db 761 AATATGTCATAGCTTCGAGATATCTTTAATAAGCGACAATGAGTTCAAGTGCAGGCAT 820
Qy 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
Db 821 TCACAGCCGAGTGTGGTTATGGCTTGCGAGCTGTATCGTTGGACAGAGTACAGCATACAG 880
Qy 221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGlu 240
Db 881 ACGATGGAAACCAAGATAAAGCTGGAATCTATCTTGGATTTTTCGAAGAAGATCTCAGTGAG 940
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 941 CACGTAGTTTCAGGGTATGCCCTTCTCGACATGTGGGTACAGCTTGTCTCTTATCATCC 1000
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
Db 1001 ACCATTGCTGAGAGTGAAGAGTGTGGAAATCTTACTCTTCCCATCATGAGCAGAAT 1060
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly 300
Db 1061 TCCCGAAAACAAATAGGCAAGTGTGAGTTGATATATATATATTAATTAATTAAGCCATTAC 1120
Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
Db 1121 TACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATTGGAAGCAAGAAATACCATTTGGAT 1180
Qy 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGluLeuAlaLysValGlnGlu 340
Db 1181 GTTGGCCATCGAGTGCAGAAACTCTACAACAACTGCCAGCTGGCTAAAGTTCAAGAA 1240
Qy 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyValAlaPheValGluPheAsp 360
Db 1241 AATACTATTGCTCTTTAAGAAATGCTGTAGTCAATGGTGCAGCTTTGTAGAAATTTGAC 1300
Qy 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
Db 1301 GTACACCTTTCAAAGGACTTTGTGCGCGTGGTATATCATGATCTTACCTGTTGTTTGACT 1360
Qy 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
Db 1361 ATGAAAAAGAAATTCGATGCTGATCCAGTTGAATTTTGAATTCAGTAAAGAAATTA 1420
Qy 401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Db 1421 ACATTTGACCAACTCCAGTTGTTAAGCTCACTCATGTGCTGACATGAAATCTAAGGAT 1480
Qy 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
Db 1481 CGGAAAGAAATCTGTGGTTTCAGGAGAAAAATTCCTTTTCAGAAAAATCAGCCATTTCTTCT 1540
Qy 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
Db 1541 CTTAAGATGGTTTAGAGTCTTTCCGAGAGATGTAGGGTTAATCAATGAAATTAATAATGG 1600
Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Db 1601 ATCTGCCAGCAAGAGGATGGAAATGTGGATGTGAATCTATCAACATATTTGACATGAAT 1660
Qy 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
1661 CTGTTTTTGGATATAATTTTAAAAAATCTGTTTAAAAAATTTCTGGGAAGAGGAGAAATAGTG 1720
501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
1721 TTTTCTTCAATTTGATGTCAGATATTTGCACAAATGGTTGGCAAAAGCAGAAACAATATCCG 1780
521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
1781 ATACTATTTTTAACTCAGGAAAAATCTGAGATTTATCTCTGAACTCATGACCTCAGATCT 1840
541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
1841 CGACAAACCCCATTCATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATAAATGTA 1900
561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
1901 CATACTAAGACTTGTCTCAGAAACCCATCTCTATATTCAGAGGCAAAAGCTAAGGACTA 1960
581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
1961 GTCATATTTCTCTGGGTGATGATACCAATGATCTCTGAAACAGAAAGAAATTTGAAGGAA 2020
601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
2021 CTTGGAGTTAATGCTCTAATTTATGATGATATATGATGATGCTGAAACCAACCAAT 2080
621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
2081 ATATTCCAAGTGGAGCAATTTGGAAACGCTTGAAGCAGGAATTTGCCAGAGCTTAAGAGCTGT 2140
641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGlyGluSerAspIleHis 660
2141 TTGTGTCCTCCTGTTAGCCGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCAT 2200
661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
2201 GTGGATGCCAACGCAATTGATAACGTGGAGAAATGCT 2236
RESULT 7
ADN05171
ID ADN05171 standard; cDNA; 5443 BP.
XX
AC ADN05171;
XX
DT 01-JUL-2004 (first entry)
XX
DE Antipsoriatic cDNA sequence #801.
XX
KW ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2004028479-A2.
XX
PD 08-APR-2004.
XX
PF 25-SEP-2003; 2003WO-US030907.
XX
PR 25-SEP-2002; 2002US-0414006P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
XX Wu TD;
XX
DR WPI: 2004-305105/28.
DR P-PSDB; ADN05172.
XX
XX New PRO nucleic acid or polypeptide, useful for preparing a
XX pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
```

PS Claim 1; SEQ ID NO 1565; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polynucleotides of the invention.
XX
SQ Sequence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 0 Length: 5443
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-10-047-855-3 (1-672) x ADN05171 (1-5443)
QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
DB 205 ATGACACCTTCTCAGGTGGCTTTGAAATAAGAGGAACTCTTTTACCAGGAGATTTT 264
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
DB 265 GCGATATGTGGAAAGCTGTGATGCTTTTGGGAAACTGGAATCCTCAAAATGCTGTGGCTCT 324
QY 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpIleValAlaThrIleValLeuSerArg 60
DB 325 CTTCCAGAGAAATGACACAGGTGAAGCATGCTATGGAAAGCAACCATTTGACTCAGTAGA 384
QY 61 GlyValSerValGlnTrpArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
DB 385 GGAATATCAGTTCAGTATCGTACTTCAAGGGTACTTTTAGAACCAAGACTATCGGT 444
QY 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
DB 445 GGTCCATGTCAAGTATAGTTCACAAGTGGGAGACTCATCTACACCAAGCATCAATAACC 504
QY 101 ProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisGlyValGlu 120
DB 505 CCTTTAGAAAGCGAAATATTATTGACGATGGCAATTTGGAAATCCACATGGTGTGA 564
QY 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
DB 565 ACTCTGATCTCGATGGCTGACATGTCAGACTGAAATAGATTAGCTTTGCTATTTCT 624
QY 141 GluLysProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
DB 625 GAAAAACCTCTCTGTGCAATAACCAAGAAAAAATTAATAAATCTAGATTAGGGTGAAG 684
QY 161 LeuThrLeuGluGlyLeuGluAspAspAspArgValSerProThrValLeuHis 180
DB 685 CTGACACTAGAGGCTGGAGGAAGATGACGATAGGATGATCTCCCACTGTACTCCAC 744
QY 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
DB 745 AAAATGTCATATAGCTTGGAGATATCTTAAATAGCGACATGATGATTCAGTGCCAGCAT 804
QY 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
DB 805 TCACAGCGGAGTGTGGTTATGGCTTGCAGCTGATCGTTGGACAGAGTACAGTACAG 864
QY 221 ThrMetGluProAspAsnLeuGluIlePheAspPheGluGluAspLeuSerGlu 240
DB 865 ACGATGGAAACCATGAACTCTGGAACTAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAG 924
QY 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
DB 925 CAGTAGTTCAGGGTGATGCCCTTCTGGACATGTGGTACAGCTTGTCTCTTATCATCC 984
QY 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280

DB 985 ACCATTGCTGAGAGTGGAAAGAGTGTGGAAATCTTACTCTTCCCATCATGACGAAAT 1044
QY 281 SerAtqLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
DB 1045 TCCCGGAAACAATAGGCAAGAGTGAGATTGACTATATTAATTAATTAAGCCATTACAGGA 1104
QY 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
DB 1105 TACAGTTGTGACATGAAATCTTTCATTTTCCAAGTATTGGAAGCCAAGATACCATTTGAT 1164
QY 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
DB 1165 GTTGGCCATCGAGGTGACGAAACTCTACAACAACATGCCAGCTGGCTTAAGTTCAAGAA 1224
QY 341 AsnThrIleAlaSerLeuArgAsnAlaLaSerHisGlyAlaAlaPheValGluPheAsp 360
DB 1225 AATACTATTGCTTCTTTAAGAAATGCTGCTAGTCATGGTGCAGCCCTTTGTAGAAATTGAC 1284
QY 361 ValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
DB 1285 GTACACCTTTCAAAGGACTTTGTGCCGCTGGTATATCATGATCTTACCTGTTGTTGACT 1344
QY 381 MetLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
DB 1345 ATGAAAGAGAAATTTGATGCTGATCCAGTTGAATATTATTGAAATTCAGTAAAGAAATTA 1404
QY 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
DB 1405 ACATTTGACCACTCCAGTTGTTAAAGCTCCTCATGTGCTGCATGCAATCTAAGGAT 1464
QY 421 ArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPheProSer 440
DB 1465 CGGAAAGAAATCTGTGCTTCAGGAGGAAATTCCTTTTCAGAAATCAGCACTTCTCTCT 1524
QY 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
DB 1525 CTTAAGATGGTTTATGAGTCTTTTGCCAGAGAGATGTAGGGTTTAAACATTTGAAATG 1584
QY 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
DB 1585 ATCTGCCACAAAGGATGGAATGTGGATGTGTAATCTTATCAACATATTTTGCATGAAT 1644
QY 481 LeuPheLeuAspIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
DB 1645 CTGTTTTTCGATATATATTTTAAAAACTGTTTTAGAAAAATTCGGGAAGAGGAGAAATG 1704
QY 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
DB 1705 TTTTCTTCATTTGATGTCAGATATTTGCACAATGGTTTCGGCAAAAGCAGAACAAATATCC 1764
QY 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
DB 1765 ATACTATTTTAACTCAGGAAATCTGAGATTTATCTGAACTCATGACCTCATGATCT 1824
QY 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnVal 560
DB 1825 CGGACAAACCCCATTCGAATGAGCTTTGACAGTTTGAATAATCTACTGGGATAAATGTA 1884
QY 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
DB 1885 CATACTGAAAGACTTGTCTCAGAAACCCATCTATATTCAAGAGGCAAAAGCTAAGGAGCTA 1944
QY 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
DB 1945 GTCATATTTCTGCTGGGGTGATGATACCAATGATCTCTGAAACACAGAGGAAATGAAGGA 2004
QY 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
DB 2005 CTTGGAGTTAATGGTCTAATTTATGATAGATATATGATTTGGATGCTGAACCAACCAAT 2064
QY 621 IlePheGlnValGluGlnLeuGluArgLysGlnLeuProGluLeuLysSerCys 640

Db 2065 ATATTCCAGTGGAGCAATTGGAAACGCTGAGCAGGAATTGCAGAGCTTAAGAGCTGT 2124
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Dd 2125 TTGTGTCCACTGTAGCGGTTTGTCCCTCACTCTTTGTGTGGGAGTCTGATATCCAT 2184
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Dd 2185 GTGGATGCCAACGGCAATTGATAACGTGGAGAACTGCT 2220

RESULT 8

ADSF74320
ID ADSF74320 standard; cDNA; 5443 BP.
XX
AC ADSF74320;
XX
DT 16-DEC-2004 (first entry)
XX
DE PRO83903 cDNA clone DNA327983, role in immune-related disease.
XX
KW PRO83903; Crohn's disease; rheumatoid arthritis; gastrointestinal-gen.;
KW antirheumatic; antiarthritic; psoriasis; antipsoriatic; gene; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH 190..2223
CDS /*tag= a
FT /product= "PRO83903"
FT /partial
FT /note= "No start codon"

XX WO2004081199-A2.

XX 23-SEP-2004.

XX 10-MAR-2004; 2004WO-US007862.

XX 11-MAR-2003; 2003US-0454025P.

XX (GETH) GENENTECH INC.

XX Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;

XX WPI; 2004-668955/65.

XX P-PSDB; ADSF74321.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid
PT arthritis.

XX Claim 1; SEQ ID NO 39; 166pp; English.

XX The present sequence is of cDNA clone DNA327983 encoding novel human PRO
CC polypeptide PRO83903. The invention provides newly identified and
CC isolated nucleotide sequences encoding polypeptides referred to as PRO
CC polypeptides that are useful in the diagnosis and treatment of immune-
CC related diseases. Microarray analysis showed that DNA327983 is up-
CC regulated 1.5-fold in lesional skin as compared to non-lesional skin from
CC psoriasis patients, up-regulated 1.3-fold in colon samples from Crohn's
CC disease patients as compared to normal colon and up-regulated 1.3-fold in
CC white blood cells from rheumatoid arthritis patients as compared to those
CC from healthy donors. It is also down-regulated 1.5-fold upon activation
CC of CD4 T cells with CD28 or ICAM and down-regulated 2-fold upon
CC activation of monocytes with LPS. PRO83903 can be used in a claimed
CC method of identifying a compound that inhibits expression of the gene
CC encoding it. The candidate compound is especially an antisense nucleic
CC acid. The PRO polypeptide, its antagonist or an antibody that binds the
CC polypeptide are used in claimed methods for the alleviation or diagnosis
CC of rheumatoid arthritis, Crohn's disease and psoriasis. A vector
CC comprising the present nucleic acid can be used to transform a host cell,
CC especially a CHO cell, Escherichia coli or yeast, for production of the
CC PRO polypeptide.

XX Sequence 5443 BP; 1544 A; 1034 C; 1149 G; 1716 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 0 Length: 5443
Score: 3537.00 Matches: 672
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dd: 13 Gaps: 0

US-10-047-855-3 (1-672) x ADSF74320 (1-5443)

Qy 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Dd 205 ATGACACCTTCTCAGGTTCCTTTGGAATTAAGAGGAACCTTTTACCAGGAGAAGTTTTT 264
Qy 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40
Dd 265 GCATATGTGAAGCTGTGATGCTTTGGGAAACCTGGAATCCTCAAATGCTGTGGCTCTT 324
Qy 41 LeuProGluAsnAspThrGlyGluSerMetLeuTrpIysAlaThrIleValLeuSerArg 60
Dd 325 CTTCCAGAGAATGACACAGGTGAAGCATGCTATGGAAGCAACCACTTTGACTCAGTAGA 384
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProIlyThrIleGly 80
Dd 385 GGAGTATCAGTTCAGTATCCTACTTCAAGGGTACTTTTATAGAACCAAGACTATCGGT 444
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Dd 445 GGTCCATGTCAGTGATAGTTCAAGTGGGAGACTCATCTCAACACCACGATCAATAAAC 504
Qy 101 ProLeuGluSerGluIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Dd 505 CCTTTAGAAAACGGAATTTATTTACGATGGGACAAATTTGGAATCCCAATGGTGTGAA 564
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Dd 565 ACTCTGGATTCTGGATGGCTGACATGTCAGACTGAATTAAGATTACGTTTGCATTATCT 624
Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Dd 625 GAAAAACCTCTGTGTCATTAACCAAGAAAAAATTAATAAATACTAGATTTAGGGTGAAG 684
Qy 161 LeuThrLeuGluGlyLeuGluGluAspAspAspArgValSerProThrValLeuHis 180
Dd 685 CTGACACTAGAAAGCCCTGGAGGAAGATGACATGATAGGGTATCTCCCACTGTACTCCAC 744
Qy 181 LysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHis 200
Dd 745 AAAATGTCATAGCTTGGAGATATCCTTAATAGCGACAATGAGTTCAAGTGCAGGCAT 804
Qy 201 SerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
Dd 805 TCACAGCCGAGTGTGGTTATGGCTTGAGCTGATCGTTGGACAGAGTACAGCATACAG 864
Qy 221 ThrMetGluProAspAsnLeuGluLeuIlePheAspPhePheGluGluAspLeuSerGlu 240
Dd 865 ACGATGGAACCAAGATTAACCTGGAACCTAATCTTTGATTTTTCGAAGAAGATCTCAGTGAG 924
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Dd 925 CAGGTAGTTACGGGTGATGCCCTTCTCGACATGTGGGTACAGCTTGTCTCTATCATCC 984
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
Dd 985 ACCATTGCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGAGCGAAAT 1044
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeuProGly 300
Dd 1045 TCCCGGAAAAACAATAGGCAAGTGAGAGTTGACTATATATTAATTATTAAAGCCATTACCAGGA 1104


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QY 301 TyrSerCysAspMetIysSerSerPheSerLysTyTrrIysProArgIlePProLeuAsp 320
Db 1105 TACAGTTGTGACATGAATCTTCATTTTCAAGTATTGGAGCCAAAGAAATACCATTTGGAT 1164
QY 321 ValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 1165 GTTGGCCATCGAGTGCAGGAACTCTACACAACTGCCAGCTGGCTAAAGTTCAAGAA 1224
QY 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAsp 360
Db 1225 AATACATTATGCTCTCTTTAAGAAATGCTGTAGTCATGGTGCAGCCCTTGTAGAAATTTGAC 1284
QY 361 ValHisLeuSerIysAspPheValProValValTyrHisAspLeuThrCysCysLeuThr 380
Db 1285 GTACACCTTTCAAGAGCTTTGTGCCGCTGTATATCATGATCTTACCTGTGTGTTGACT 1344
QY 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400
Db 1345 ATGAAAAGAAATTTGATGCTGATCCAGTTGAATTTATTTGAAATTCAGTAAAGAATTA 1404
QY 401 ThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Db 1405 ACATTTTGACCAACTCCAGTTGTTTAAAGCTCCTCATGTGACTGCACCTGAAATCTAAGGAT 1464
QY 421 ArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnPropheProSer 440
Db 1465 CGGAAAGAAATCTGTGTTTTCAGGAGGAAATTCCTTTTCAGAAATCAGCCATTTCTCTCT 1524
QY 441 LeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrp 460
Db 1525 CTTAAGATGTTTTCAGTCTTTTGCAGAGAGATGTAGGGTTTACATTTGAATTAATATGG 1584
QY 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Db 1585 ATCTGCCAGCAAGGATGGAATGTGGATGTTAACTTATCAACATATTTTGACATGAAT 1644
QY 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgIleVal 500
Db 1645 CTGTTTTTGGATATAATTTTAAAACTGTTTTAGAAAAATTCGGGAGAGGAGATAGTG 1704
QY 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1705 TTTTCTTCATTTGATGCAGATATTTGCACAATGGTTCCGCAAAAGCAGAACAAATATCCG 1764
QY 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1765 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTGAACTCATGACCTCAGATCT 1824
QY 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnVal 560
Db 1825 CGGACAAACCCCATTCGAATGAGCTTTGCACAGCTTTGAAAAATCTACTGGGGATAAATGTA 1884
QY 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1885 CATACTGAAGACTTGTCTGAAACCCCATCTATTTATTCAGAGAGCAAAAGCTAAGGACTA 1944
QY 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1945 GTCATATTTCTGCTGGGTGATGATACCAATGATCTCTGAAAAACAGAGGAAATTAAGGAA 2004
QY 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 2005 CTTGGAGTTAAATGGTCTAATTTATGATAGATATATGATGATGCTGCAACCAACAAAT 2064
QY 621 IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
Db 2065 ATATTCAGAGTGAGCAATTTGGAACCCCTGGAACAGGAAATTCAGAGCTTTAAGACTGT 2124
QY 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2125 TTGTGTCCCACTGTTAGCGCTTTGTTTCCCTCATCTTTGTGTGGGAGTCTGATATCCAT 2184
QY 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
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Db 2185 GTGGATGCCAACGGCATTGATAACGTGGAGATGCT 2220

RESULT 9

ABV23741
ID ABV23741 standard; cDNA; 3498 BP.
XX
AC ABV23741;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23732.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005171.
XX
PR 17-FEB-2000; 2000US-0183319P.
PR 16-MAR-2000; 2000US-0189862P.
PR 25-MAY-2000; 2000US-0207454P.
PR 09-JUN-2000; 2000US-0211314P.
PR 18-JUL-2000; 2000US-0219007P.
PR 13-DEC-2000; 2000US-0255281P.
XX
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
PS Claim 1; Page 4356-4357; 11750pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
XX
SQ Sequence 3498 BP; 1103 A; 609 C; 736 G; 1040 T; 0 U; 10 Other;

Alignment Scores:
Pred. No.: 0 Length: 3498
Score: 3509.00 Matches: 671
Percent Similarity: 99.85% Conservative: 0
Best Local Similarity: 99.85% Mismatches: 1
Query Match: 99.21% Indels: 1
DB: 5 Gaps: 0

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QY 1 MetThrProSerGlnValAlaPheGluIleArgGlyThrLeuLeuProGlyGluValPhe 20
Db 221 ATGACACCTTCTCAGGTTCCTTTGAAATTAAGAGGAACTCTTTTACAGAGAGATTTT 280
QY 21 AlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAlaValAlaLeu 40

Db 281 GCGATATGTGAAGCTGTGATGCTTTGGGAAATCGGAATCCTCAAAATGCTGTGGCTCTT 340
Qy 41 LeuProGluAenAspThrGlyGluSerMetLeuTrpLysAlaThrIleValLeuSerArg 60
Db 341 CTTCCAGAGAATGACACAGGGTGAAGCATGTAATGGAAAGCAACCAATTGTACTCAGTAGA 400
Qy 61 GlyValSerValGlnTyrArgTyrPheLysGlyTyrPheLeuGluProLysThrIleGly 80
Db 401 GGAGTATCAGTTTCAGTATCGTACTCTCAAGGGGACTTTTTAGAACCAAGAGACTATCGGT 460
Qy 81 GlyProCysGlnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
Db 461 GGTCCATGTCGAAGTGAATGTTTCAAGTGGGAGACTCATCTACCAACCAAGCATCAATACC 520
Qy 101 ProLeuGluSerGluIleIleAaspAspGlyGlnPheGlyIleHisAsnGlyValGlu 120
Db 521 CTTTAGAAAGCGAAATTAATTATTGACGATGGACAATTTGGAAATCCCAATGGTGTGA 580
Qy 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSer 140
Db 581 ACTCTGGATTCGTGGTGTGACATGTGACACTGAAATTAAGATTACGTTTGCATATTCT 640
Qy 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
Db 641 GAAAAACCTCCTGTGTCAATAACCAAGAAATAATTAATAAATCTAGATTAGGGTGAAG 700
Qy 161 LeuThrLeuGluGlyLeuGluAspAspAspArgValSerProThrValLeuHis 180
Db 701 CTGACACTAGAAAGCGCTGGAGAGATGACGATGATAGGGTATCTCCCACTGTACTCCAC 760
Qy 181 LysMetSerAsnSerLeuGluIleSerLeuLeuSerAspAsnGluPheLysCysArgHis 200
Db 761 AAAATGTCCATAGCTTGGAGATATCCTTAATAGCGACAATGAGTTCAAGTGCAGGCAT 820
Qy 201 SerGlnProGluCysGlyTyrClyLeuGlnProAspArgTrpThrGluTyrSerIleGln 220
Db 821 TCACAGCGGAGTGTGGTATGGCTTGCAGCCGTGATCGTTGGACAGAGTACAGCATACAG 880
Qy 221 ThrMetGluProAspAsnLeuGluIlePheAspPhePheGluGluAspLeuSerGlu 240
Db 881 ACGATGGAAACCAAGATAACCTGGAATCTATCTTTGATTTTCGAAGAAGATCTCAGTGAG 940
Qy 241 HisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSer 260
Db 941 CACGTAGTTTCAGGGTATGCCCTTCTCGACATGTGGGTACAGCTTGTCTCTTATCATCC 1000
Qy 261 ThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsn 280
Db 1001 ACCATTGTCTGAGAGTGGAAAGAGTGTGGAATTTCTTACTCTTCCCATCATGAGCGAAAT 1060
Qy 281 SerArgLysThrIleGlyLysValArgValAspTyrIleIleLysProLeuProGly 300
Db 1061 TCCCGGAAACCAATAGGCAAGTGGAGTTGACTATATTAATTAATTAAGCCATTACCGGA 1120
Qy 301 TyrSerCysAspMetLysSerSerPheSerLysTyrTrpLysProArgIleProLeuAsp 320
Db 1121 TACAGTTGTGACATGAATCTTCAATTTTCCAAAGTATGGAAAGCAAGATACCAATGGAT 1180
Qy 321 ValGlyHisArgGlyAlaGlyLysSerThrThrAlaGlnLeuAlaLysValGlnGlu 340
Db 1181 GTTGGCCATCGAGTGCAGGAACTCTACAACAACCTGCCCGAGCTGGCTTAAGTTCAAGAA 1240
Qy 341 AsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyValAlaPheValGluPheAsp 360
Db 1241 AATACTATTGCTTCTTTAAGAAATGCTGTAGTCAATGGTGGAGCCCTTGTAGAAATTGAC 1300
Qy 361 ValHisLeuSerLysAspPheValProValTyrHisAspLeuThrCysCysLeuThr 380
Db 1301 GTACACCTTTCAAGGACCTTTGGCCGGTGGTATATCATGATCTTACCTGTGTGTGACT 1360
Qy 381 MetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeu 400

Db 1361 ATGAA-AAGAAATTTGATGCTGATCCAGTTGAATTAATTTGAAATTCAGTAAAGAAATTA 1419
Qy 401 ThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAsp 420
Db 1420 ACAATTTGACCAACTCCAGTTGTTAAAGCTCACTCATGTGACTGCACCTGAATCTAAGGAT 1479
Qy 421 ArgLysGluSerValValGlnGluLysSerPheSerGluAsnGlnProPheProSer 440
Db 1480 CGGAAAGAAATCTGTGTTTCAAGGAGAAATTCCTTTTTCAGAAATCAGCCATTTCTCTCT 1539
Qy 441 LeuLysMetValLeuGluSerLeuProGluLysValGlyPheAsnIleGluIleLysVal 460
Db 1540 CTTAAGATGTTTTAGAGTCTTTTCCAGAGAGATGTAGGGTTTAAACATTTGAAATTAATAATGG 1599
Qy 461 IleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsn 480
Db 1600 ATCTGCCAGCAAGAGGATGGAATGTGGATGGTAACCTTATCAACATATTTTGACATGAAT 1659
Qy 481 LeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArgIleVal 500
Db 1660 CTGTTTTTGGATATAATTTTAAAACTGTTTAAAGAAATTCCTGGGAAAGAGAGAAATAGTG 1719
Qy 501 PheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrPro 520
Db 1720 TTTTCTTCTCATTTGATGTCAGATATTTGCACAAATGTTCCGCAAAAGACAGAAATATCCG 1779
Qy 521 IleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSer 540
Db 1780 ATACTATTTTAACTCAAGGAAATCTGAGATTTATCTGNACTCATGGACCTCAGATCT 1839
Qy 541 ArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIleAsnVal 560
Db 1840 CGGACAAACCCCATTTGCAATGAGCTTTGCACAGTTTGAAATCTTACTGGGATAAATGTA 1899
Qy 561 HisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeu 580
Db 1900 CATACTGAAGACTTGTCTCAGAAACCCATCTCTATATTCAGAGGCAAAAGCTTAAGGGACTA 1959
Qy 581 ValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeuLysGlu 600
Db 1960 GTCATATTTCTGCTGGGGTATGATACCAATGATCCTGAAACACAGAGAAATTAAGAGAA 2019
Qy 601 LeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsn 620
Db 2020 CTTGAGATTAAATGCTCTAAATTTATGATAGGATATATGATGATGCTGCAACCAACAAAT 2079
Qy 621 IlePheGlnValGluGlnLeuGluArgLysGlnGluLeuProGluLeuLysSerCys 640
Db 2080 ATATTCCAAGTGGAGCAATTTGGAACGCTGAAGCAGGAAATTTGCCAGAGCTTTAAGAGCTGT 2139
Qy 641 LeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAspIleHis 660
Db 2140 TTGTGTCCACTGTGTAGCCGCTTTGTCCTCATCTTTGTGTGGGAGTCTGTATATCCAT 2199
Qy 661 ValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2200 GTGGATGCCAACGGCAATTCATTAACGTGGAGAAATGCT 2235
RESULT 10
ADJ57938
ID ADJ57938 standard; cDNA; 3381 BP.
XX
AC ADJ57938;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat NARC 16 cDNA.
XX
KW Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
KW lung disease; cirrhosis; hepatitis; atherosclerosis;
KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;

drug screening; gene therapy; cytostatic; hepatotropic; neurotropic; cerebrotective; dermatological; virucide; neuroprotective; phosphatidylglycerol phosphate synthase; PGP synthase; rat; ss.

Rattus norvegicus.
US2004009553-A1.
15-JAN-2004.
30-APR-2003; 2003US-00426776.
27-SEP-1999; 99US-00406045.
22-OCT-1999; 99US-0161188P.
31-JAN-2000; 2000US-00495823.
28-FEB-2000; 2000US-0185517P.
20-OCT-2000; 2000US-00692785.
31-JAN-2001; 2001US-00773426.
28-FEB-2001; 2001US-00795691.
31-OCT-2001; 2001US-0335003P.
31-OCT-2001; 2001US-0335037P.
25-MAR-2002; 2002US-00105992.
28-AUG-2002; 2002US-00229662.
30-OCT-2002; 2002US-00284014.
30-OCT-2002; 2002US-00284059.
09-DEC-2002; 2002US-00314881.
(MILL-) MILLENNIUM PHARM INC.
Glucksmann MA, Williamson MJ, Tsai P, Rudolph-Owen LA;
Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
WPI; 2004-090469/09.
New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 22436, 23553, NARC SCI or NARC I) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer, atherosclerosis or AIDS.
Claim 1; SEQ ID NO 39; 260pp; English.
The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or 32222. The invention is useful in diagnosing, preventing or treating disorders such as cancer, lung diseases, cirrhosis, hepatitis, atherosclerosis, myocardial infarction, inflammation, anaemia, glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency syndrome), Parkinson's disease, Alzheimer's disease, stroke and dermatitis. These may also be used in drug screening. The invention is also useful in gene therapy. The present sequence is rat neuronal apoptosis regulated candidate (NARC) cDNA.
SQ Sequence 3381 BP; 990 A; 689 C; 729 G; 973 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.58e-291 Length: 3381
Score: 2965.50 Matches: 571
Percent Similarity: 90.76% Conservative: 38
Best Local Similarity: 85.10% Mismatches: 33
Query Match: 83.84% Indels: 29
DB: 12 Gaps: 6
US-10-047-855-3 (1-672) x ADJ57938 (1-3381)
QY 1 Met-Thr-Pro-Ser-Gln-Val-Ala-Phe-Glu-Ile-Arg-Gly-Thr-Leu-Leu-Pro-Gly-Glu-Val-Phe 20
Db 186 ATGACACCTTCTCAGGTACCTTTGAATTAAGGAACTCTTTTACGAGAGGCTTT 245
QY 21 Ala-Ile-Cys-Gly-Ser-Cys-Asp-Ala-Leu-Gly-Asn-Trp-Asn-Pro-Gln-Ala-Val-Ala-Leu 40

Db 246 GCAATGTGTGGAACTGTGATCCCTTGGAAATCTGGAGTCTCTCAAAATCTGTGCTCT --- 302
QY 41 Leu-Pro-Glu-Asn-Asp-Thr-Gly-Glu-Ser-Met-Leu-Tyr-Lys-Ala-Thr-Ile-Val-Leu-Ser-Arg 60
Db 303 CTTACTGAGAGTGAGACAGCGGAAAGT---GTATGGAAAGCAGTGATGTTCTTCTAGTAGA 359
QY 61 Gly-Val-Ser-Val-Gln-Tyr-Arg-Tyr-Phe-Lys-Gly-Tyr-Phe-Leu-Glu-Pro-Lys-Thr-Ile-Gly 80
Db 360 GGAATGTCGCTGAAGTACCGCTACTTTCAGAGGCTGCTTTTATAGAACCAAGACTATCGGT 419
QY 81 Gly-Pro-Cys-Gln-Val-Ile-Val-His-Tyr-Trp-Glu-Thr-His-Leu-Gln-Pro-Arg-Ser-Ile-Thr 100
Db 420 GGTCCATGTCAAGTCATAGTTCACAAGTGGGAGACTCATCTACAACACGATCAATAAC 479
QY 101 Pro-Leu-Glu-Ser-Glu-Ile-Ile-Leu-Asp-Gly-Gln-Phe-Gly-Ile-His-Asn-Gly-Val-Glu 120
Db 480 CTTTAGAAAACGAATCATTTATTCGATGAGCAATTTGGAAATCCACAATGGTGTGAA 539
QY 121 Thr-Leu-Asp-Ser-Gly-Trp-Leu-Thr-Cys-Gln-Thr-Glu-Ile-Arg-Leu-Arg-Leu-His-Tyr-Ser 140
Db 540 ACACTGGATTCTGGATGGCTTACCTGTGACACTGAAATTAAGACTGCGTCTGCATTTTCT 599
QY 141 Glu-Lys-Pro-Val-Ser-Ile-Thr-Lys-Lys-Leu-Lys-Lys-Ser-Arg-Phe-Arg-Val-Lys 160
Db 600 GAGAAACCTCTCTGTTTCAATTACCAAGAAAAAGTTCAAAAAATCTAGATTTAGGGTAAAG 659
QY 161 Leu-Thr-Leu-Glu-Gly-Leu-Glu-----Asp-Asp-Asp-Arg-Val-Ser-Pro-Thr-Val 178
Db 660 CTTACACTAGAGGGTCTGGAGGAAGATGATGACGAGATGATGAAGCATCTCCACTGTT 719
QY 179 Leu-His-Lys-Met-Ser-Asn-Ser-Leu-Glu-Ile-Ser-Leu-Ile-Ser-Asp-Asn-Glu-Phe-Lys-Cys 198
Db 720 CTTCAAGATGCTCCAAATAGCTGGAGATATCTTAAATAGTGACAAATGAGTCAAGTGC 779
QY 199 Arg-His-Ser-Gln-Pro-Glu-Cys-Gly-Tyr-Gly-Leu-Gln-Pro-Asp-Arg-Trp-Thr-Glu-Tyr-Ser 218
Db 780 AGGCACCTCACAGCCAGAAATGTGGTATGGCTTTACAGCCTGACCGCTGGACAGATGACAGC 839
QY 219 Ile-Gln-Thr-Met-Glu-Pro-Asp-Ser-Leu-Glu-Ile-Phe-Asp-Phe-Glu-Glu-Asp-Leu 238
Db 840 ATACAGACAAATGGAGCCGGACAACTTGAACCTCATCTTTGACTTTTTTGGAGGAAGATCTC 899
QY 239 Ser-Glu-His-Val-Val-Gln-Gly-Asp-Ala-Leu-Pro-Gly-His-Val-Gly-Thr-Ala-Cys-Leu-Leu 258
Db 900 AGTGAGCATGTAGTCAGGGTGTGTTCTTCTCTGGACATGTGGGACACAGCATGCGCTCCTG 959
QY 259 Ser-Ser-Thr-Ile-Ala-Glu-Ser-Gly-Lys-Ser-Ala-Gly-Ile-Leu-Thr-Leu-Pro-Ile-Met-Ser 278
Db 960 TCATCTACCATTTGCTGAGAGTGAGAGAGCGCTGGAATCCTTACTCTTCCCATCATGAGC 1019
QY 279 Arg-Asn-Ser-Arg-Lys-Thr-Ile-Gly-Lys-Val-Arg-Val-Asp-Tyr-Ile-Ile-Ile-Lys-Pro-Leu 298
Db 1020 AAGAGTTCCAGAAAAACATATAGCAAGATGATGAGTTGATTTTATCATCATCAAGCCATTA 1079
QY 299 Pro-Gly-Tyr-Ser-Cys-Asp-Met-Lys-Ser-Ser-Phe-Ser-Lys-Tyr-Trp-Lys-Pro-Arg-Ile-Pro 318
Db 1080 CCAGGATATAGTTGTTCTATGCGAGTCTTCATCTCCAAGTATTTGGAACCAAGAAATACCA 1139
QY 319 Leu-Asp-Val-Gly-His-Arg-Gly-Ala-Gly-Asn-Ser-Thr-Thr-Thr-Ala-Gln-Leu-Ala-Lys-Val 338
Db 1140 CTGGATGTTGGACATCGTGGTCAGGGAACCTCAACAACTGCCCAAGCTGGCTAAAGTA 1199
QY 339 Gln-Glu-Asn-Thr-Ile-Ala-Ser-Leu-Arg-Ala-Ile-Ser-His-Gly-Ile-Ala-Phe-Val-Glu 358
Db 1200 CAGGAAAAATACTATTGCTTCTTTAAGAAATGTCGCCAGCATGGTGGTGGTGGAA 1259
QY 359 Phe-Asp-Val-His-Leu-Ser-Lys-Asp-Phe-Val-Pro-Val-Val-Tyr-His-Asp-Leu-Thr-Cys-Cys 378
Db 1260 TTTGATGTCACCTTTCAAGGACTTAGTGCTGTAGTGTATCATGATCTACCTGCTGT 1319
QY 379 Leu-Thr-Met-Lys-Lys-Phe-Asp-Ala-Leu-Glu-Leu-Phe-Glu-Ile-Pro-Val-Lys 398

nervous system disorder; autoimmune disorder; inflammation; allergy; ds.

Homo sapiens.

WO200174836-A1.

11-OCT-2001.

30-MAR-2001; 2001WO-US010472.

31-MAR-2000; 2000US-00540217.

23-AUG-2000; 2000US-00649167.

30-NOV-2000; 2000US-0250583P.

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;

WPI; 2001-626375/72.

New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cancer and increasing hematopoiesis, stem cell survival and bone growth and remodeling.

Claim 1; Page 254-255; 380pp; English.

The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a DNA of the invention

Sequence 2477 BP; 681 A; 500 C; 642 G; 654 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	7.42e-278	Length:	2477
Scores:	2829.50	Matches:	573
Percent Similarity:	79.97%	Conservative:	14
Best Local Similarity:	78.07%	Mismatches:	36
Query Match:	80.00%	Indels:	111
DB:	5	Gaps:	11

US-10-047-855-3 (1-672) x ABA09667 (1-2477)

QY 18 GluValPheAlaIleCysGlySerCysAspAlaLeuGlyAsnTrpAsnProGlnAsnAla 37

DB 369 GAAATTTTGGGATATGTGGAGCTGTGATCTTTGGGAAACTGGATCTCTCAAAATGCT 428

QY 38 ValAlaLeuLeuProGluAsnAspThrGlyGluSerMetLeuTrpLysAlaThrIleVal 57

DB 429 GTGGCTCTTCTCCAGAGAAATGACACAGTGANAGCATGCTATGGAAGCAACCATTTGTA 488

QY 58 LeuSerArgGlyValSerValGlnTrpArgTrpPheLysGlyTrpPheLeuGluProLys 77

DB 489 CTCAGTAGAGGATGATCAGTTTCAGTATCGTACTTCAAAGGCTACTTTTGAACCAAG 548

QY 78 ThrIleGlyGlyProCysGlnValIleValHisLysTrpGluThrHisLeuGln---Pro 96

DB 549 -----GAAACATTCATCATCGGTGACTTCTTGTAACTTTTCACTTTTCA 590

QY 97 ArgSerIleThrProLeuGluSerGluIleIleIleAspAspGlyGlnPhe----- 113

DB 591 AGTTCT-----TCAGTTCTCTTGTTCAGACTGACAGTTCTCTGGGAGG 638

QY 113 ----- 113

1320 TTAACATGAAAGAAATATGAGCTGATCCAGTTGAATTTTGAATCCCGTAAAG 1379

QY 399 GluLeuThrPheAspGlnLeuGlnLeuLeuLysLeuThrHisValThrAlaLeuLysSer 418

DB 1380 GAATTAACATTCGACCAACTCCAGTTATTGAGCTTTCTCATGTGACTGCACTAAAAACC 1439

QY 419 LysAspArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProphe 438

DB 1440 AAGACCAAGAAACAATGTATGGCTGAGGAGGAAATTTCTTTCTGAAACCAACCATTT 1499

QY 439 ProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIle 458

DB 1500 CTTCTCTTAAGATGGTTTAGAGTCATGTCGAGAAATGTAGGATTTAATATAGAATA 1559

QY 459 LysTrpIleCysGlnGlnAtqAspGlyMetTrpAspGlyAsnLeuSerThrTrpPheAsp 478

DB 1560 AAATGGATTTCCCAACACAGGATGGAGTATGGAGCGCAACTTATCGACATATTTGAT 1619

QY 479 MetAsnLeuPheLeuAspIleIleLeuLysThrValLeuGluAsnSerGlyLysArgArg 498

DB 1620 ATGAATGCATTTTGGATATAATTTTAAAAACTGTTTAGAAAAATTCGGGAGAGGAGA 1679

QY 499 IleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLys 518

DB 1680 ATAGTATTTTCTTCATTTTGCAGACATCTGTACATGGTTTCGCAGAAACAAACAAA 1739

QY 519 TyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTrpProGluLeuMetAspLeu 538

DB 1740 TATCCATATATTTTGGACCAAGGAAGTCTGACATTTACCTTGAACTCATGGACCTC 1799

QY 539 ArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIle 558

DB 1800 AGATCTCGGACAAACCCATTGCAATGAGCTTTGCACAGTTTGAAAAATTTTGGGGATA 1859

QY 559 AsnValHisThrGluAspLeuLeuArgAsnProSerTrpIleGlnGluAlaLysAlaLys 578

DB 1860 AATGCCCATCTAGAGATCTCTTGAAGAACCCATCTATGTCCAAGAGGCAAAAGATAG 1919

QY 579 GlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgLysLeu 598

DB 1920 GGATTTGGTATATTTCTGCTGGGGTGATGATACATGATCTCTGAAAACAGAGGAACTG 1979

QY 599 LysGluLeuGlyValAsnGlyLeuIleTrpAspArgIleTrpAspTrpMetProGluGln 618

DB 1980 AAGGAATTTGGAGTAAATGGTCTAATATATGATAGTAT----- 2018

QY 619 ProAsnIlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeu----- 634

DB 2019 -----TTGTTTTTTGTAAGAAATCTCCATGGAAATTTGTTCAACAGCTGATGTTTATCTA 2072

QY 635 -----ProGluLeuLysSer-----CysLeuCys 642

DB 2073 TTTTAACTATTTTAAATTAGATAGTTTAGCTTAAAGTTTATCTTGACACTGTGACCTT 2132

QY 643 ProThrValSerArgPheValProSerSerLeu 653

DB 2133 TCCAGGTGTGGATATGTCAAGGCCACTTA 2165

RESULT 11

ABA09667

ID ABA09667 standard; DNA; 2477 BP.

XX ABA09667;

AC ABA09667;

XX 15-JAN-2002 (first entry)

DE Human bone marrow expressed oligonucleotide SEQ ID NO: 176.

XX Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;

KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;

KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;

KW antitumor; fungicide; antidiabetic; antiasthmatic; antiallergic;

KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;

Db 639 GACATAGACAGACCAAACTAAGTCTCTGGGCGAGGGCTGGGGTTTGAATGGGCT 698
Qy 114 -----Gly11eHisAsnGly 118
Db 699 ATAGAGCTATGCATGGCAGTCAAAGAGGATGTTTCGACAGGAAGTAGGAAGCCATATAGG 758
Qy 119 ---ValGluThrLeuAspSerGlyTrpLeuThrCysGln-----ThrGlu 132
Db 759 TTACTTCTCTGATGTTGCCATGGCAATTTGTAACACTGTCGTGGCACTGATGGAGTGAGCA 818
Qy 133 IleArgLeu---ArgLeuHis----- 138
Db 819 GTGAGATGACACAGAGGTCACTCTCATTCGCCATCTTGGTTTGGCTACTGTGCTAGTGGG 878
Qy 139 TyrSerGluLysProValSer----- 146
Db 879 TTCTCCTTGGAGCCTTGTGTGAATAATGAGTGTGGGGCCTCTTCTGCAGAGGTGCAACAG 938
Qy 147 -----IleThrLysLysLysLeuLysLysSer-----ArgPheArg 158
Db 939 GGCTTCGTGTTTCATCATCTGCCTCCTCTCTCTCATATTGCACTGAGGCCAAAGG 998
Qy 159 ValLysLeuThrLeuGluGlyLeuGluGluAspAspAspAspValSerProThrVal 178
Db 999 GTGAAGCTGACACTAGAAGCCTGGAGAGATGACGATGATAGGTATCTCCCACTGTA 1058
Qy 179 LeuHisLysMetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCys 198
Db 1059 CTCACAAATGTCCAAATAGCTTGGAGATATCTTAATAAGCGACAAATGAGTTCAAGTGC 1118
Qy 199 ArgHisSerGlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSer 218
Db 1119 AGGCATTTCACAGCGGAGTGTGTTATGCTTGCAGCCTGATCGTTGGACAGAGTACAGC 1178
Qy 219 IleGlnThrMetGluProAspAsnLeuGluIlePheAspPheGluGluAspLeu 238
Db 1179 ATACAGACCATGGAACCATACCTGGAACTAATCTTTGATTTTTTCGAAGAAGATCTC 1238
Qy 239 SerGluHisValValGlnGlyAspAlaLeuProGlyHisValGlyThrAlaCysLeuLeu 258
Db 1239 AGTGACACGTAGTTTCAGGGTGATGCCCTTCTCTGGACATGTGGGTACAGCTTGTCTTTA 1298
Qy 259 SerSerThrIleAlaGluSerGlyLysSerAlaGlyIleLeuThrLeuProIleMetSer 278
Db 1299 TCATCCACCAATGCTCAGAGTGGAAAGAGTGTGGAAATCTTACTCTTCCCATCATGAGC 1358
Qy 279 ArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLeu 298
Db 1359 AGAAATTCCTCCGAAAAACAATAGCAAGTGAGAGTTGACTATATATAATTATTAAAGCCATTA 1418
Qy 299 ProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTriplysProArgIlePro 318
Db 1419 CCAGGATACAGTTGTGACATGAATCTTCAATTTCCAGTATTGGAGGCCAAGATACCA 1478
Qy 319 LeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysVal 338
Db 1479 TTGGATGTTGGCCATCGAGTGCAGGAAACTCTACAAACACTGCCCGAGCTGGCTAAAGTT 1538
Qy 339 GlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGlu 358
Db 1539 CAAGAAATATACATTCTCTTTAAGAAATGTGCTAGTCATGGTGCAGCTTTGAGAA 1598
Qy 359 PheAspValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCys 378
Db 1599 TTTGAGTACACCTTTCAAGAGACTTTGTGGCGGTGATATCATGATCTTACCTGTGTT 1658
Qy 379 LeuThrMetLysLysLysPheAspAlaAspProValGluLeuPheGluIleProValLys 398
Db 1659 TTGACTATCAAAAGAAATTTGATGCTGATCCAGTTGAATTTATTTGAAATTCAGTAAAA 1718
Qy 399 GluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSer 418
Db 1719 GAATTAACATTTGACCAACTCCAGTTGTTTAAAGCTCACTCATGTGACTGCACTGAATCT 1778

Qy 419 LysAspArgLysGluSerValValGlnGluGluAsnSerPheSerGluAsnGlnProphe 438
Db 1779 AAGGATCGGAAGAATCTGTGTTTCAGGAGGAAATTCCTTTTCAGAAAATCAGCCATTT 1838
Qy 439 ProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIle 458
Db 1839 CCTTCTCTTAAGATG----- 1853
Qy 459 LysTyrIleCysGlnGluAspGlyMetTyrAspGlyAsnLeuSerThrTyrPheAsp 478
Db 1854 -----GATGGAATGTGGATGGTAACTTATCAACATATTTTGAC 1892
Qy 479 MetAsnLeuPheLeuAspIleLeuLysThrValLeuGluAsnSerGlyLysArgArg 498
Db 1893 ATGAATCTGTTTTCGATATAATTTTAAAAACTGTTTAAAGAAATTCCTGGAGAGAGAGA 1952
Qy 499 IleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLys 518
Db 1953 ATAGTGTGTTTCTTCATTTTGCATGATATTTTCACAATGGTTTCGGCAAAAGAGACAAA 2012
Qy 519 TyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeu 538
Db 2013 TATCCGATACTATTTTAACTCAAGGAAATCTGAGATTTATCTTGAATCTCATGGACCTC 2072
Qy 539 ArgSerArgThrThrProIleAlaMetSerPheAlaGlnPheGluAsnLeuGlyIle 558
Db 2073 AGATCTCGACAAACCCCATTCGAATGAGCTTTGCACAGTTTGMAAATCTACTGGGGATA 2132
Qy 559 AsnValHisThrGluAspLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLys 578
Db 2133 AATGTACATACTGAAAGACTTGTCTCAGAAACCCATCTATATTCAAGAGGCAAAAGCTAAG 2192
Qy 579 GlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgArgLysLeu 598
Db 2193 GGACTAGTCATATTTCTGTGGGGTGATGATACCAATGATCTCTGAAAAACAGAGAAATTTG 2252
Qy 599 LysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGln 618
Db 2253 AAGGAACTTGGAGTTTAATGGTCTAATTTATGATAGATATATGATTTGGATGCTGAACAA 2312
Qy 619 ProAsnIlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLys 638
Db 2313 CCAAAATATATTCCAAGTGGAGCAATTTGGAAACCCCTGAAAGCAGAGAAATTCAGAGCTTAA 2372
Qy 639 SerCysLeuCysProThrValSerArgPheValProSerSerLeuCysGlyGluSerAsp 658
Db 2373 AGCTGTTTGTGTCCCACTGTTAGCCGCTTTGTTCCCTCATCTTTGTGGGGAGTCTGAT 2432
Qy 659 IleHisValAspAlaAsnGlyIleAspAsnValGluAsnAla 672
Db 2433 ATCCATGTGGATGCCAACGGCATTGATAACGTGGAGATGCT 2474

RESULT 12

AAD06007

ID AAD06007 standard; DNA; 2738 BP.

XX AAD06007;

XX AAD06007;

XX 31-JUL-2001 (first entry)

XX Human neuronal apoptosis regulated candidate (NARC) 9B DNA.

XX Human;

XX Human; neuronal apoptosis regulated candidate 9B; NARC 9B; cytoskeletal;

XX chromosome mapping; gene therapy; antisense therapy; lung disorder;

XX central nervous system disorder; apoptosis; spleen disorder; angina;

XX tuberculosis; Goodpasture's syndrome; liver disorder; jaundice;

XX infectious disorder; brain disorder; cerebral oedema; gonorrhoea;

XX heart disorder; kidney disorder; glomerulonephritis; testes; virucide;

XX epidiidymis disorder; skeletal muscle disorder; pancreatic disorder;

XX diabetes; cytoprotective; immunostimulant; tumour; antiinflammatory;

XX antimicrobial; neuroprotective; gynaecological; ds.

XX

XX

OS Homo sapiens.
 XX WO200131007-A2.
 XX
 XX 03-MAY-2001.
 XX
 XX 20-OCT-2000; 2000WO-US029132.
 XX
 XX 22-OCT-1999; 99US-0161188P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 XX
 XX Chiang LW;
 XX
 XX WPI; 2001-308641/32.
 DR
 XX
 XX Rat brain polypeptides, nucleic acids and antibodies, useful for
 PT diagnosis and treatment of central nervous system disorders and disorders
 PT associated with aberrant apoptosis.
 XX
 XX Claim 1; Page 146; 161pp; English.
 PS
 XX The invention relates to human homologues of neuronal apoptosis regulated
 CC candidate (NARC) nucleic acid molecules and proteins derived from rat
 CC brain and programmed cell death libraries. The nucleic acids of the
 CC brain are useful for assaying the presence of a nucleic acid molecule
 CC and for chromosome mapping. They are also used in gene therapy and
 CC antisense therapy. The NARC sequences are useful for treating central
 CC nervous system disorders and disorders involving aberrant apoptosis, for
 CC inducing an immune response and for isolating binding partners. Diseases
 CC treated include spleen disorders (e.g. tuberculosis and congestive
 CC splenomegaly), lung disorders (e.g. adult respiratory distress syndrome,
 CC Goodpasture's syndrome and bronchial asthma), liver disorders (e.g.
 CC jaundice and hepatic failure), infectious disorders (e.g. viral
 CC hepatitis), brain disorders (e.g. cerebral oedema, hypertensive
 CC encephalopathy and hydrocephalus), heart disorders (e.g. heart failure,
 CC angina and myocardial infarction), kidney disorders (e.g. cysts and
 CC glomerulonephritis), testes and epididymis disorders (e.g. gonorrhoea and
 CC syphilis), skeletal muscle disorders (e.g. tumours) and pancreatic
 CC disorders (e.g. pancreatitis and diabetes). The present sequence is human
 CC neuronal apoptosis regulated candidate (NARC) 9B DNA
 XX
 XX Sequence 2738 BP; 880 A; 450 C; 540 G; 868 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 1.76e-249 Length: 2738
 Score: 2552.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 72.15% Indels: 0
 DB: 4 Gaps: 0

US-10-047-855-3 (1-672) x AAD06007 (1-2738)

Qy 187 GluIleSerLeuIleSerAspAenGluPheLysCysAeArgHisSerGlnProGluCysGly 206
 Db 18 GAGATATCTTATATAGCGCATATGATGTTCAAGTGCAGGCATTACAGCGGAGTGTGT 77
 Qy 207 TyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAspAen 226
 Db 78 TATGGCTTCAGCGCTGATCGTTGGACAGAGTACAGCATACAGACGATGGACAGATAAC 137
 Qy 227 LeuGluLeuIlePheAspPheGluGluAspLeuSerGluHisValGlnGlyAsp 246
 Db 138 CTGGAACATACTTGTGATTTTTCGAAGAAGATCTCAGTGAGGCACGTAGTTCAGGGTAT 197
 Qy 247 AlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGly 266
 Db 198 GCCCTTCTCGACATGTGGGTACAGCTTGCTCTTATCATCCACCATTCGTGAGGTGGA 257
 Qy 267 LysSerAlaGlyIleLeuThrLeuProIleMetSerArgAenSerArgLysThrIleGly 286
 Db 258 AAGAGTGTGGAATCTTACTCTTCCCATCATGACGAGAAATTCCTCCGGAACATAGGC 317

Qy 287 LysValArgValAspTyrIleIleLysProLeuProGlyTyrSerCysAspMetLys 306
 Db 318 AAAGTGAGAGTTGACTATATTAATTAATTAAGCCNTTACCAGGATACAGTTGTGACATGAA 377
 Qy 307 SerSerPheSerLysTyrTrpLysProArgLleProLeuAspValGlyHisArgGlyAla 326
 Db 378 TCTTCAATTTTCAAGTATTTGGAAGCCAAAGATACCATTTGGATGTTGGCCATCGAGGTGCA 437
 Qy 327 GlyAenSerThrThrAlaGlnLeuAlalysValGlnGluAasnThrIleAlaSerLeu 346
 Db 438 GGAACCTCTACAACTGCCAGCTGGTAAAGTTCAAGAAATFACATATTCTTCTTTA 497
 Qy 347 ArgAenAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAsp 366
 Db 498 AGAAATGCTGCTAGTCATGGTGCAGCCITTTAGAAATTTGACGTACACCTTTCAAGGAC 557
 Qy 367 PheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAsp 386
 Db 558 TTTGTGCCCGGTGATATCATGATCTTACCTGTGTGTGACTATGAAAAAGAAATTTGAT 617
 Qy 387 AlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGln 406
 Db 618 GCTGATCCAGTTGAATTTTGAATTTCCAGTAAAGAAATTAACATTTGACCACTCCAG 677
 Qy 407 LeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValVal 426
 Db 678 TTGTTAAAGCTCACTCATGTGACTGCTGAAATCTTAAGATCGGAAAGAAATCTGTGGTT 737
 Qy 427 GlnGluGluAasnSerPheSerGluAenGlnProPheProSerLeuLysMetValLeuGlu 446
 Db 738 CAGAGGAAATTCCTTTTCAGAAATCAGCCATTTCTTCTTAAGATGTTTTAGAG 797
 Qy 447 SerLeuProGluAspValGlyPheAenIleGluIleLysTrpIleCysGlnGlnArgAsp 466
 Db 798 TCTTTGCCAGAGATGTAGGGTTTAAACATTTGAATAAAATGGAATCTGCCACCAAGGGAT 857
 Qy 467 GlyMetTrpAspGlyAenLeuSerThrTyrPheAspMetAasnLeuPheLeuAspIleIle 486
 Db 858 GGAATGTGGGATGGTAACTTATCAACATATTTTGACATGAATCTGTTTTGGATATAAT 917
 Qy 487 LeuLysThrValLeuGluAasnSerGlyLysArgArgIleValPheSerSerPheAspAla 506
 Db 918 TTAAAAACTGTTTTAGAAAAATTTCTGGAGAGGAGAGATAGTGTTCCTTCTATTGTATGCA 977
 Qy 507 AspIleCysThrMetValArgGlnLysGlnAasnLysTyrProIleLeuPheLeuThrGln 526
 Db 978 GATATTTGCACAAATGGTTTCGCAAAAGCAGAAACAAATATCCGATACATATTTTAACTCAA 1037
 Qy 527 GlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAla 546
 Db 1038 GGAATAATCTGAGATTTTATCTGAACTCATGGACCTCAGATCTCGACACACCCCATTTGCA 1097
 Qy 547 MetSerPheAlaGlnPheGluAasnLeuGlyIleAenValHisThrGluAspLeuLeu 566
 Db 1098 ATGAGCTTTGCACAGTTTGAAAAATCTACTGGGATAAAATGTATACATCTGGAAGCTTGGCTC 1157
 Qy 567 ArgAenProSerTyrIleGlnGluAlalysAlalysGlyLeuValIlePheCysTrpGly 586
 Db 1158 AGAAACCCATCTCTATATTCAAGAGGCAAAAGCTAAGGGACTAGTCATATTTCTGGGGGT 1217
 Qy 587 AspAspThrAenAspProGluAasnArgArgLysLeuLysGluLeuGlyValAasnGlyLeu 606
 Db 1218 GATGATACCAATGATCTCTGAAAAACAGAAGGAAATTTGAAGGAACTTGGAGTTTAATGCTCTA 1277
 Qy 607 IleTyrAspArgIleTyrAspTrpMetProGluGlnProAasnIlePheGlnValGluGln 626
 Db 1278 ATTTATGATAGGATATATGATTTGGATGCTGAAACCAACAAATATATTTCCAAAGTGAGCAA 1337
 Qy 627 LeuGluArgLeuLysGlnLeuProGluLeuProLysSerCysLeuCysProThrValSer 646
 Db 1338 TTGGAAACGCTTGAAGCAGGAATTTGCCAGAGCTTAAAGCTGTTTGTGTGCCACTGTTAGC 1397

QY 647 ArgPheValProSerSerLeuCysGlyLeuSerAspIleHisValAspAlaAsnGlyIle 666
 Db 1398 CGTTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCCATGCGATGCCAAGCGCAT 1457
 QY 667 AspAsnValGluAsnAla 672
 Db 1458 GATAACGTGGAGATGCT 1475

RESULT 13

ADJ57931
 ID ADJ57931 standard; cDNA; 2738 BP.

AC ADJ57931;

DT 06-MAY-2004 (first entry)

XX Human NARC 9 cDNA.

XX Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
 KW lung disease; cirrhosis; hepatitis; atherosclerosis;
 KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
 KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
 KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;
 KW drug screening; gene therapy; cytostatic; hepatotropic; neurotropic;
 KW cerebroprotective; dermatological; virucide; neuroprotective;
 KW phosphatidylglycerolphosphate synthase; PGP synthase; human; ss.

XX Homo sapiens.

OS US2004009553-A1.

PN 15-JAN-2004.

PD 30-APR-2003; 2003US-00426776.

PF 27-SEP-1999; 99US-00406045.

PR 22-OCT-1999; 99US-0161188P.

PR 31-JAN-2000; 2000US-00495823.

PR 28-FEB-2000; 2000US-0185517P.

PR 20-OCT-2000; 2000US-00692785.

PR 31-JAN-2001; 2001US-00773426.

PR 28-FEB-2001; 2001US-00795691.

PR 31-OCT-2001; 2001US-0335003P.

PR 31-OCT-2001; 2001US-0335037P.

PR 25-MAR-2002; 2002US-00105992.

PR 28-AUG-2002; 2002US-00229662.

PR 30-OCT-2002; 2002US-00284014.

PR 30-OCT-2002; 2002US-00284059.

PR 09-DEC-2002; 2002US-00314881.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA, Williamson MJ, Tsai F, Rudolph-Owen LA;

PI Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;

XX WPI; 2004-090469/09.

XX New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413, 22438, 23553, NARC SCI or NARC 1) useful for diagnosing, preventing or treating disorders associated with the protein, e.g. cancer, atherosclerosis or AIDS.

XX Claim 1; SEQ ID NO 32; 260pp; English.

XX The present invention provides isolated nucleic acid molecules and proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SCI, NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4, NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20, NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C, NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or 32222. The invention is useful in diagnosing, preventing or treating disorders such as cancer, lung diseases, cirrhosis, hepatitis, atherosclerosis, myocardial infarction, inflammation, anaemia,

CC glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency syndrome), Parkinson's disease, Alzheimer's disease, stroke and dermatitis. These may also be used in drug screening. The invention is also useful in gene therapy. The present sequence is human neuronal CC apoptosis regulated candidate (NARC) cDNA.

XX Sequence 2738 BP; 880 A; 450 C; 540 G; 868 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.76e-249 Length: 2738
 Score: 2552.00 Matches: 486
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 72.15% Indels: 0
 DB: 12 Gaps: 0

US-10-047-855-3 (1-672) x ADJ57931 (1-2738)

QY 187 GluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSerGlnProGluCysGly 206
 Db 18 GAGATATCCTTAATAAGCCGACCAATGAGTTCAAAGTGCGAGCATTCACAGCCGGAGTGTGGT 77
 QY 207 TyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThrMetGluProAspAsn 226
 Db 78 TATGGCTTCAGCCTGATCGTTGGACAGAGTACAGCATACAGACATGGAACACAGATAAC 137
 QY 227 LeuGluLeuIlePheAspPhePheGluGluAspLeuSerGluHisValGlnGlyAsp 246
 Db 138 CTGGAACATAATCTTTGATTTTTTCGAAGAAGATCTCAGTGAGCACCGTAGTTACAGGTGAT 197
 QY 247 AlaLeuProGlyHisValGlyThrAlaCysLeuLeuSerSerThrIleAlaGluSerGly 266
 Db 198 GCCCTTCTCGACATGTGGGTACAGCTGTCTTATCATCCACCATGTCTGAGAGTGA 257
 QY 267 LysSerAlaGlyIleLeuThrLeuProIleMetSerArgAsnSerArgLysThrIleGly 286
 Db 258 AAGAGTCTGGAAATCTTACTCTTCCCATCAGCAGAGAAATTCGCGGAAAAAACAATAGGC 317
 QY 287 LysValArgValAspTyrIleIleLysProLeuProGlyTyrSerCysAspMetLys 306
 Db 318 AAGTGAGAGTTGACTATATATTAAGCCATTACAGGATACAGTTGTGACATGAAA 377
 QY 307 SerSerPheSerLysTyrTrpLysProArgIleProLeuAspValGlyHisArgGlyAla 326
 Db 378 TCTTCATTTTCCAAGTATTGGAAGCCAGAAATACCATTTGGATGTGGCCATCCAGGTGCA 437
 QY 327 GlyAsnSerThrThrAlaGlnLeuAlaLysValGlnGluAsnThrIleAlaSerLeu 346
 Db 438 GGAAACTCTACAACTGCCAGCTGGCTAAAGTTCAAGAAATACTATTGCTTCTTTA 497
 QY 347 ArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspValHisLeuSerLysAsp 366
 Db 498 AGAATGCTGCTAGTCATCGTGCAGCCTTTGTAGAAATTTGACGTACACCTTTCAAGGAC 557
 QY 367 PheValProValValTyrHisAspLeuThrCysCysLeuThrMetLysLysLysPheAsp 386
 Db 558 TTTGTGCGCGTGGTATATCATGATCTTACCTGTGTGTGCTATGAAAGAAATTTGAT 617
 QY 387 AlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAspGlnLeuGln 406
 Db 618 GCTGATCCAGTTGAATTTTGAATTTCCAGTAAAGAAATTAACATTTGACCACTCCAG 677
 QY 407 LeuLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGluSerValVal 426
 Db 678 TTGTTAAAGCTCCTCATGTGACTGCACCTGAAATCTAAGATCGGAAGAAATCTGTGTT 737
 QY 427 GlnGluGluAsnSerPheSerGluAsnGlnProPheProSerSerLeuLysMetValLeuGlu 446
 Db 738 CAGGAGGAAAAATTCCTTTTCAGAAAAATCAGCAATTCCTTCTTAAGATGGTTTTAGAG 797
 QY 447 SerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGlnGlnArgAsp 466
 Db 798 TCTTTGCCAGAGATGTAGGTTTAAATTTGAATTAATAATGGAATCTGCCAGCAAGGAT 857

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Qy 467 GlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeuAspIleile 486
Db 858 GGAATGTGGATGTAATATATCAACATATTTTGCATGATCTGTTTGGATATATTT 917
Qy 487 LeuLysThrValLeuGluAsnSerGlyLysArgArgIleValPheSerSerPheAspAla 506
Db 918 TTAANAATCTGTTTGTAGAAAATCTGGAGAGGAGATAGTGTCTTCTCATTTGATGCA 977
Qy 507 AspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPheLeuThrGln 526
Db 978 GATATTTGCACATGTTTGGCAAAAGCAGAAACAAATATCCGATCTATTTTAACTCAA 1037
Qy 527 GlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThrProIleAla 546
Db 1038 GGAAATCTGAGATTTATCTCTGAACTCATGTGACCTCAGATCTCGACAAACCCCATTTGCA 1097
Qy 547 MetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGluAspLeuLeu 566
Db 1098 ATGAGCTTTGCACAGTTTGAATAATCTACTGGGGATAAATGATACATCTGAAAGACTTGCTC 1157
Qy 567 ArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePheCysTrpGly 586
Db 1158 AGAAACCATCTATATTCAGAGGCAAAAGCTAAGGACTAGTCATATTTCTGCTGGGT 1217
Qy 587 AspAspThrAsnAspProGluAsnArgArgLysLeuLysGluLeuGlyValAsnGlyLeu 606
Db 1218 GATGATACCAATGATCTCTGAAACAGAGGAATTTGAAGGAACCTTGGAGTTTAATGGTCTA 1277
Qy 607 IleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnIlePheGlnValGluGln 626
Db 1278 ATTTATGATAGATATATGATTGGAGTCTGAAACCAACCAATATATTTCCAAGTGGAGCA 1337
Qy 627 LeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCysLeuCysProThrValSer 646
Db 1338 TTGGAACGCTGACAGAGGAATGTCAGAGCTTAAAGACTGTTTGTGCTCCACTGTTAGC 1397
Qy 647 ArgPheValProSerSerLeuCysGlyGluSerAspIleHisValAspAlaAsnGlyIle 666
Db 1398 CGCTTTGTTCCCTCATCTTTGTGTGGGAGTCTGATATCCATGTGGATGCCAACGGCAT 1457
Qy 667 AspAsnValGluAsnAla 672
Db 1458 GATAACGTGGAGATGCT 1475

RESULT 14
ABA09583
ID ABA09583 standard; DNA; 1978 BP.
XX AC ABA09583;
XX DT 15-JAN-2002 (first entry)
XX DE Human bone marrow expressed oligonucleotide SEQ ID NO: 9.
XX KW Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnery;
XX KW antinflammatory; antibacterial; immunosuppressive; vasotropic; cancer;
XX KW antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
XX KW antitumor; fungicide; antidiabetic; antisthmatic; antiallergic;
XX KW immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
XX KW nervous system disorder; autoimmune disorder; inflammation; allergy; ds.
XX OS Homo sapiens.
XX XX WO200174836-A1.
XX PN 11-OCT-2001.
XX PD 30-MAR-2001; 2001WO-US010472.
XX PF 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PR 30-NOV-2000; 2000US-0250583P.
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XX (HYSE-) HYSEQ INC.
XX PA
XX Tang YT, Liu C, Drmanac RT, Ford JE, Boyle BJ;
XX PI
XX WPI; 2001-626375/72.
XX DR P-PSDB; ABB12339.
XX PT New bone marrow-expressed nucleic acids and polypeptides, useful for
XX PT diagnosis, treatment of inflammatory, autoimmune, neurological, cancer
XX PT and increasing hematopoiesis, stem cell survival and bone growth and
XX PT remodeling.
XX PS Claim 1; Page 163; 380pp; English.
XX CC The present invention relates to bone marrow expressed polynucleotides
XX CC and proteins. These sequences can be used in the treatment of
XX CC inflammatory conditions (eg arthritis, Crohn's disease), cancer, central
XX CC and peripheral nervous system diseases and neuropathies, such as
XX CC Alzheimer's, Parkinson's and Huntington's diseases, spinal cord
XX CC disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid
XX CC cell disorders, platelet disorders, stem cell disorders, bone
XX CC degenerative disorders, autoimmune disorders, for example multiple
XX CC sclerosis, diabetes and arthritis, viral and bacterial infections,
XX CC allergies and blood coagulation disorders. The present sequence is a DNA
XX CC of the invention
XX SQ Sequence 1978 BP; 633 A; 329 C; 417 G; 599 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3,25e-238 Length: 1978
Score: 2439.50 Matches: 489
Percent Similarity: 94.84% Conservative: 7
Best Local Similarity: 93.50% Mismatches: 18
Query Match: 68.97% Indels: 9
DB: 5 Gaps: 3

US-10-047-855-3 (1-672) x ABA09583 (1-1978)
Qy 102 LeuGluSerGluIleIleIleAspAspGlyGlnPheGlyIleHisAsnGlyValGluThr 121
Db 339 CTAGAAAGCGAAATTAATTATGACGATGGACAATTTTGAATCCCAATGGTGTGAAACT 398
Qy 122 LeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgLeuHisTyrSerGlu 141
Db 399 CTGGATTCGTGATGGCTGACATGTCAGACTGAATATAGATTACGTTTGCATTATTCGAA 458
Qy 142 LysProProValSerIleThrLysLysLysLysSerArgPheArgValLysLeu 161
Db 459 AAACCTCTGTGTCAATAACCAAGAAAAATTAATAAATCTAGATTTAGGTTGAAGCTG 518
Qy 162 ThrLeuGluGlyLeuGluGluAspAspArgValSerProThrValIleHisLys 181
Db 519 ACACCTAGAAAGCGCTGGAGGAAGATGACGATGATAGGGTATCTCCACTGTATCTCCACAA 578
Qy 182 MetSerAsnSerLeuGluIleSerLeuIleSerAspAsnGluPheLysCysArgHisSer 201
Db 579 ATGTCCAATAGCTGGAGATATCTTTAATAAGCGCAATAGTTTCAAGTCAGGCAATCA 638
Qy 202 GlnProGluCysGlyTyrGlyLeuGlnProAspArgTrpThrGluTyrSerIleGlnThr 221
Db 639 CAGCCGGAGTGTGGTTATGGCTTGCAGCTGATCGTTGGACAGAGTACAGATACAGACG 698
Qy 222 MetGluProAspAsnLeuGluLeuIlePheAspPheGluGluAspLeuSerGluHis 241
Db 699 ATGGAACAGAGATAACCTCGAACTAATCTTTGAAAGAAAGATCTCTAGTGAGCAC 758
Qy 242 ---ValValGlnGlyAspAlaLeuPro-GlyHisValGlyThrAlaCys-LeuLeu---S 259
Db 759 CGTAAAGTTACGGGGGTGATGCCCTTCTGGGACATGTGGGTACAGCTTGTCTCTTATCC 818
Qy 259 erSerThrIleAlaGluSer--GlyLysSerAlaGlyIleLeuThrLeuProIleMetSe 278
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Db 819 ATCCACCATTCGTGAAGAGTGGAAAGAGTGTGGAATCTTACTCTTCCCATCATGAG 878
Qy 278 rArgAsnSerArgLysThrIleGlyLysValArgValAspTyrIleIleIleLysProLe 298
Db 879 CAGAAATTCGCGAAACAATAGCAAGGAGAGTTGACTATATATATTAATTAAGCCATT 938
Qy 298 uProGlyTyrSerCysAspMetLysSerSerPheSerLysTyrTTrpLysProArgIlePr 318
Db 939 ACCAGATACAGTTGTGACATGAATCTTCATTTTCCAAGTATVTTGAAGCAAGATACC 998
Qy 318 oLeuAspValGlyHisArgGlyAlaGlyAsnSerThrThrAlaGlnLeuAlaLysVa 338
Db 999 ATTGGATGTGGCCATCGAGGGCAGAAACTCTACAACTGCCAGCTGCTGCTAAAGT 1058
Qy 338 lGlnGluAsnThrIleAlaSerLeuArgAsnAlaLaSerHisGlyAlaAlaPheValG 358
Db 1059 TCAAGAAATACTATTGCTTCTTTAAGAAATGCTGTAGTCATGGCGACGCTTTGTAGA 1118
Qy 358 uPheAspValHisLeuSerLysAspPheValProValValTyrHisAspLeuThrCysCy 378
Db 1119 ATTTGACGTACACCTTTCAAAGGACTTTGTGCCCGTGGTATATCATGATCTTACCTGTTG 1178
Qy 378 sLeuThrMetLysLysPheAspAlaAspProValGluLeuPheGluIleProValLy 398
Db 1179 CTTGACTATGAAAGAAATTTGATGCTGATCCAGTTGAATTAATTTGAAATTCAGTAAA 1238
Qy 398 sGluLeuThrPheAspGlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSe 418
Db 1239 AGAATTAACATTTTGACCACTCCAGTGTGTAAAGCTCACTCAITGCTGACTGCACTGAATC 1298
Qy 418 rLysAspArgLysGluSerValValGlnGluAsnSerPheSerGluAsnGlnProPh 438
Db 1299 TAAGGATCGAAAGAATCTGTGTTTCAGGAGGAAATTCCTTTTCAGAAATCAGCCATT 1358
Qy 438 eProSerLeuLysMetValLeuGluSerLeuProGluAspValGlyPheAsnIleGlu 458
Db 1359 TCCTCTCTTAAGATGGTTTTAGAGTCTTTGCCAGAGATGTAGGGTTTAAACATTGAAT 1418
Qy 458 eLysTrpIleCysGlnGlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAs 478
Db 1419 AAAATGGATCTGCCAGCAAGGATGGATGTGGATGTAATTAATCAACATATTTTGA 1478
Qy 478 pMetAsnLeuPheLeuAspIleIleLysThrValLeuGluAsnSerGlyLysArgAr 498
Db 1479 CATGAATCTGTTTTTGATATATAATTTTAAAACTGTTTAAAAAATCTCGGAAGAGGAG 1538
Qy 498 gIleValPheSerSerPheAspAlaAspIleCysThrMetValArgGlnLysGlnLys 518
Db 1539 AATAGTGTGTTTCTTCATTTGATCAGATATTTGCACAATGGTTTCGCAAAAGCAGAACAA 1598
Qy 518 sTyrProIleLeuPheLeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspL 538
Db 1599 ATATCGATACATATTTTAACTCAGAAATGTGTAGATTGATGCCAGTGCATGACT 1658
Qy 538 euArgSerArgThrThrProIleAlaMetSerPheAla-GlnPheGluAsnLeuLeuGly 557
Db 1659 TCAGGTGTGCGAACACCCCATTCGAATGAGCTTTGCACGAGTTGAAAATCTGCTCGCG 1718
Qy 558 IleAsnValHisThrGluAspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAla 577
Db 1719 ATAAATGTACATCTGAAGACTTGTCTCAGAAACCCATCTCATATTCAGAGGCAAAAGCT 1778
Qy 578 LysGlyLeuValIlePheCysTrpGlyAspAspThrAsnAspProGluAsnArgAgLys 597
Db 1779 AAGGGACTAGTCATATCTGCTGGGTGATGATACCAATGATCTGAAAACAGAAAGAAA 1838
Qy 598 Leu---LysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMet 615
Db 1839 ATTGAAGGAAACTTGGAGTTAATGCTTAATTTATGATAGGTATTTGTTTTTCATG 1895

RESULT 15
ADJ57947
ID

ADJ57947 standard; cDNA; 2393 BP.

Alignment Scores:
Pred. No.: 6.14e-132
Score: 1399.00

Length: 2393
Matches: 261

XX AC ADJ57947;
XX DT 06-MAY-2004 (first entry)
XX DE Rat NARC 9 cDNA.
XX KW Neuronal apoptosis regulated candidate; NARC; diagnosis; cancer;
KW lung disease; cirrhosis; hepatitis; atherosclerosis;
KW myocardial infarction; inflammation; anaemia; glomerulonephritis;
KW osteoporosis; AIDS; acquired immunodeficiency syndrome;
KW Parkinson's disease; Alzheimer's disease; stroke; dermatitis;
KW drug screening; gene therapy; cytostatic; hepatotropic; nootropic;
KW cerebroprotective; dermatological; virucide; neuroprotective;
KW phosphatidylglycerolphosphate synthase; FCP synthase; rat; ss.
XX OS Rattus norvegicus.
XX PN US2004009553-A1.
XX PD 15-JAN-2004.
XX PF 30-APR-2003; 2003US-00426776.
XX PR 27-SEP-1999; 99US-00406045.
PR 22-OCT-1999; 99US-0161188P.
PR 31-JAN-2000; 2000US-00495823.
PR 28-FEB-2000; 2000US-0185517P.
PR 20-OCT-2000; 2000US-00692785.
PR 31-JAN-2001; 2001US-00773426.
PR 28-FEB-2001; 2001US-00795691.
PR 31-OCT-2001; 2001US-0335003P.
PR 31-OCT-2001; 2001US-0335037P.
PR 25-MAR-2002; 2002US-00105992.
PR 28-AUG-2002; 2002US-00229662.
PR 30-OCT-2002; 2002US-00284014.
PR 30-OCT-2002; 2002US-00284059.
PR 09-DEC-2002; 2002US-00314881.
XX (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Williamson MJ, Tsai F, Rudolph-Owen LA;
PI Kapeller-Libermann R, Meyers RE, Chiang LW, Hunter JJ;
XX WPI; 2004-090469/09.
XX PT New isolated nucleic acid molecules and polypeptides (e.g. 27411, 23413,
PT 22438, 23553, NARC SC1 or NARC 1) useful for diagnosing, preventing or
PT treating disorders associated with the protein, e.g. cancer,
PT atherosclerosis or AIDS.
XX Claim 1; SEQ ID NO 48; 260pp; English.
XX The present invention provides isolated nucleic acid molecules and
CC proteins designated 27411, 23413, 22438, 23553, 25278, 26212, NARC SC1,
CC NARC 10A, NARC 1, NARC 12, NARC 13, NARC 17, NARC 25, NARC 3, NARC 4,
CC NARC 7, NARC 8, NARC 11, NARC 14A, NARC 15, NARC 16, NARC 19, NARC 20,
CC NARC 26, NARC 27, NARC 28, NARC 30, NARC 5, NARC 6, NARC 9, NARC 10C,
CC NARC 8B, NARC 9, NARC 2A, NARC 16B, NARC 1C, NARC 1A, NARC 25, 86604 or
CC 3222. The invention is useful in diagnosing, preventing or treating
CC disorders such as cancer, lung diseases, cirrhosis, hepatitis,
CC atherosclerosis, myocardial infarction, inflammation, anaemia,
CC glomerulonephritis, osteoporosis, AIDS (acquired immunodeficiency
CC syndrome), Parkinson's disease, Alzheimer's disease, stroke and
CC dermatitis. These may also be used in drug screening. The invention is
CC also useful in gene therapy. The present sequence is rat neuronal
CC apoptosis regulated candidate (NARC) cDNA.
XX
SQ Sequence 2393 BP; 762 A; 435 C; 455 G; 741 T; 0 U; 0 Other;

Percent Similarity:	95.85%	Conservative:	16
Best Local Similarity:	90.31%	Mismatches:	12
Query Match:	39.55%	Indels:	0
DB:	12	Gaps:	0
US-10-047-855-3 (1-672) x ADJ57947 (1-2393)			
Qy	384	LysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThrPheAsp	403
Db	71	AAATATGAGCTGATCCAGTTGAAATGTTGAAATCCAGTAAAGGAATTAACATTCGAC	130
Qy	404	GlnLeuGlnLeuLysLeuThrHisValThrAlaLeuLysSerLysAspArgLysGlu	423
Db	131	CAATCCAGTTATTGAGCTTCTCATGTGACTCACTAAACACCAAGACCCAGAAACAA	190
Qy	424	SerValValGlnGluGluAAsnSerPheSerGluAAsnGlnProPheProSerLeuLysMet	443
Db	191	TGTATGGCTGAGGAGGAAAATTCCTTTTCTGAAACCAACCAATTTCTCTCTTAAAGATG	256
Qy	444	ValLeuGluSerLeuProGluAspValGlyPheAsnIleGluIleLysTrpIleCysGln	463
Db	251	GTTTTAGAGTCATTCGCCAGAAATTTAGGATTTTATATAGAAATATAAATGGATTTGCCAA	310
Qy	464	GlnArgAspGlyMetTrpAspGlyAsnLeuSerThrTyrPheAspMetAsnLeuPheLeu	483
Db	311	CACAGGGATGAGTATGTCGCGCAACTTATCGACATATTTTGATATGAATGCAATTTTGT	370
Qy	484	AspIleIleLeuLysThrValLeuGluAAsnSerGlyLysArgArgIleValPheSerSer	503
Db	371	GATATATATTTTAAAAACCTGTTTTAGAAATTCGGGAAAGAGAGATAGTATTTTCTTCA	430
Qy	504	PheAspAlaAspIleCysThrMetValArgGlnLysGlnAsnLysTyrProIleLeuPhe	523
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Qy	524	LeuThrGlnGlyLysSerGluIleTyrProGluLeuMetAspLeuArgSerArgThrThr	543
Db	491	TTGACCCCAAGGAAAGTCTGACATTTTACCCTGAACTCATGGACCTCAGATCTCGGACACA	550
Qy	544	ProIleAlaMetSerPheAlaGlnPheGluAsnLeuLeuGlyIleAsnValHisThrGlu	563
Db	551	CCCATTTGCANTGAGCTTTGCACAGTTTGAATAATTTTGGGGATAAATGCCCATACTGAA	610
Qy	564	AspLeuLeuArgAsnProSerTyrIleGlnGluAlaLysAlaLysGlyLeuValIlePhe	583
Db	611	GATCTCTTTAGAAAACCATCTATGTCCAGAGGCAAAAGATTAAGGATTTGTCATATTC	670
Qy	584	CysTrpGlyAspAspThrAsnAspProGluAAsnArgArgLysLeuLysGluLeuGlyVal	603
Db	671	TGCTGGGGTGATGATACCAATGATCTCTGAAACAGAGAGAACTGAGAGAAATTTGGAGTA	730
Qy	604	AsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGlnProAsnIlePheGln	623
Db	731	AATGGTCTAATATATGATAGGATATACGATTTGGATGCCTGAACCAACCAATATATTCCAA	790
Qy	624	ValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCysLeuCysPro	643
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Qy	644	ThrValSerArgPheValProSerLeuCysGlyGluSerAspIleHisValAspAla	663
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Qy	664	AsnGlyIleAspAAsnValGluAAsnAla	672
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Search completed: July 3, 2005, 07:07:33
Job time : 1016 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 3, 2005, 06:45:04 ; Search time 8001 Seconds
(without alignments)
4069.729 Million cell updates/sec

Title: US-10-047-855-3

Perfect score: 3537

Sequence: 1 MTPSQVAFIRGTLPLGEVF.....LCGESDIHVANDINDVENA 672

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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12: gb.sy.*

13: gb.un.*

14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3537	100.0	3206	6	AX127528 Sequence
2	3537	100.0	3206	6	AX675186 Sequence
3	3537	100.0	3265	9	BC027588 Homo sapi
4	3537	100.0	3499	6	CQ413929 Sequence

ALIGNMENTS

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DEFINITION	AX127528	Sequence 4 from Patent WO0131007.				
ACCESSION	AX127528	Sequence 4 from Patent WO0131007.				
VERSION	AX127528.1	GI:14134233				
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SOURCE		Homo sapiens				
ORGANISM		Homo sapiens				
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS		Chiang L.W.				
TITLE		Nucleic acid molecules derived from rat brain and programmed cell death models				
JOURNAL		Patent: WO 0131007-A 4 03-MAY-2001;				
FEATURES		Millennium Pharmaceuticals, Inc. (US)				
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Percent Similarity:						

Best Local Similarity: 100.00%		Mismatches: 0
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US-10-047-855-3 (1-672) x AX127528 (1-3206)		
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Qy	621	IlePheGlnValGluGlnLeuGluArgLeuLysGlnGluLeuProGluLeuLysSerCys 640
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LOCUS		
DEFINITION Sequence 4 from Patent WO02081516.		
AX675186 3206 bp DNA linear PAT 27-MAR-2003		

ACCESSION AX675186
VERSION AX675186.1 GI:29333417
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE Chiang, L.W.
AUTHORS Narciso and Narci16, programmed cell death-associated molecules and
TITLES patent: WO 02081516-A 4 17-OCT-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
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Query Match: 100.00% Indels: 0
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US-10-047-855-3 (1-672) x AX675186 (1-3206)

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DEFINITION MGC:26147 IMAGE:4827346), complete cds.
ACCESSION BC027588
VERSION BC027588.2 GI:34194199
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Ahteshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
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Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y.,
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Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Kravinsky,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 3265)
Strausberg,R.
Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 25, 2003 this sequence version replaced gi:20379525.
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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REFERENCE 1
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21000 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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AUTHORS             Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE               Genes differentially expressed in human prostate cancer and their
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JOURNAL             Patent: WO 0160860-A 23730 23-AUG-2001;
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Best Local Similarity: 100.00%      Mismatches: 0
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ACCESSION CQ497765
VERSION CQ497765.1 GI:41463401
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Schlegel, R., Endege, W.O. and Monahan, J.E.
TITLE Genes differentially expressed in human prostate cancer and their use
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Millennium Predictive Medicine, Inc. (US)
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AUTHORS	Li, J. Y., Boado, R. J. and Partridge, W. M.			
TITLE	Blood-brain barrier genomics			
JOURNAL	J. Cereb. Blood Flow Metab. 21 (1), 61-68 (2001)			
MEDLINE	21024389			
PUBMED	11149669			
REFERENCE	2 (bases 1 to 3229)			
AUTHORS	Li, J. Y., Boado, R. J. and Partridge, W. M.			
TITLE	Direct Submission			
JOURNAL	Submitted (11-FEB-2003) Medicine, UCLA, 900 Veteran Ave., Warren			
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ORIGIN

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US-10-047-855-3 (1-672) x AY233980 (1-3229)

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Db 1662 TATCCATATATTTTGGACCCAGGAAAGTCTGACATTTACCTGAACCTCATGGACCTC 1721
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Qy 599 LysGluLeuGlyValAsnGlyLeuIleTyrAspArgIleTyrAspTrpMetProGluGln 618
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LOCUS Homo sapiens chromosome 7 clone XXFOS-87042G10, WORKING DRAFT
DEFINITION SEQUENCE, 3 unordered pieces.
ACCESSION AC144439
VERSION AC144439.1 GI:29893792
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 39694)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 39694)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2003) Genome Sequencing Center, Washington University School of Medicine, 444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT ----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: H AA087042G10
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 39167 bases at least Q40
Consensus quality: 39319 bases at least Q30
Consensus quality: 39366 bases at least Q20
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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* as soon as it is available and the accession number will
* be preserved.
* 1 7028: contig of 7028 bp in length
* 7029 7128: gap of unknown length
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* 16223 16822: gap of unknown length
* 16823 39694: contig of 22772 bp in length.
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Percent Similarity: 78.50% Conservative: 17
Best Local Similarity: 76.38% Mismatches: 35
Query Match: 84.61% Indels: 139
DB: 2 Gaps: 6
US-10-047-855-3 (1-672) x AC144439 (1-39694)
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REFERENCE
AUTHORS
TITLE
JOURNAL

4 (bases 1 to 149259)
Waterston,R.H.
Direct Submission
Submitted (28-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

5 (bases 1 to 149259)
Waterston,R.
Direct Submission
Submitted (03-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

6 (bases 1 to 149259)
Waterston,R.H.
Direct Submission
Submitted (13-APR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

7 (bases 1 to 149259)
Waterston,R.
Direct Submission
Submitted (20-APR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE
AUTHORS
TITLE
JOURNAL

8 (bases 1 to 149259)
Wilson,R.
Direct Submission
Submitted (08-OCT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Apr 13, 2002 this sequence version replaced gi:19774659.

COMMENT

----- Genomes Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics

Center project name: H_NH1217F02

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI Chromosome 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/FTP/CHR7>, send
<mailto:regreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong
and coworkers at <http://www.chori.org>

VECTOR: pBACe3.6

Location/Qualifiers

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/mol_type="genomic DNA"

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Pred. No.: 4,1e-248 Length: 149259
Score: 2992.50 Matches: 611
Percent Similarity: 78.50% Conservative: 17
Best Local Similarity: 76.38% Mismatches: 35
Query Match: 84.61% Indels: 139
DB: 9 Gaps: 6

US-10-047-855-3 (1-672) x AC099654 (1-149259)

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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 6671)
 AUTHORS Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-2003) MIPS, Ingolstaedter Landstr.1, D-85764
 Neuherberg, GERMANY
 COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
 This clone (DKFZp451O1715) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
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QY 342 ThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheValGluPheAspVal 361
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QY 382 LysLysPheAspAlaAspProValGluLeuPheGluIleProValLysGluLeuThr 401
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AC150686.1 GI:50872649
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
Wilson,R.K.
1 (bases 1 to 160762)
The sequence of Pan troglodytes clone
Unpublished
2 (bases 1 to 160762)
Wilson,R.K.
Direct Submission
Submitted (31-JUL-2004) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Project Information -----
Center project name: C.AB0549B03
----- Summary Statistics -----
Sequencing vector: M13; 0%
Chemistry: Dye-primer ET; 0% of reads
Assembly: Dye-terminator Big Dye; 100% of reads
Consensus quality: 156619 bases at least Q40
Consensus quality: 157310 bases at least Q30
Consensus quality: 157914 bases at least Q20
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 8714: contig of 8714 bp in length
* 8715 8814: gap of unknown length
* 8815 35261: contig of 26447 bp in length
* 35262 35361: gap of unknown length
* 35362 62200: contig of 26839 bp in length
* 62201 62300: gap of unknown length
* 62301 114137: contig of 51837 bp in length
* 114138 114237: gap of unknown length
* 114238 158156: contig of 43919 bp in length
* 158157 158256: gap of unknown length
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QY      41  LeuProGluAsnAspThrGly-Glu----- 48
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DEFINITION	Sequence 13981 from Patent WO02068579.	linear	PAT 03-FEB-2004
ACCESSION	CQ728047		
VERSION	CQ728047.1	GI:42295769	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.		
FEATURES	Kits, such as nucleic acid arrays, comprising a majority of		
source	humanexons or transcripts, for detecting expression and other uses		
	thereof		
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QY	337	sValGlnGluAsnThrIleAlaSerLeuArgAsnAlaAlaSerHisGlyAlaAlaPheVa	357
Db	867	AGTTCAAGAAATAATCTATTGCTTTTAAAGAAATGCTGTAGTCATGGTGCACCTTTGT	926
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ORIGIN

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Percent Similarity: 87.11% Conservative: 29
Best Local Similarity: 82.81% Mismatches: 18
Query Match: 81.92% Indels: 71
DB: 10 Gaps: 3

US-10-047-855-3 (1-672) x BC033408 (1-3174)

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DB 253 ATTAATGAAACAGAGAGGAGACAGTGTGTTGTGGAAGACAGTGTCTCTCAATAGA 312
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DB 313 GGAGTGTGAGTGAAGTACCGTACTTTCAGAGGCTGCTTTTAGAA----- 357
QY 81 GlyProCysClnValIleValHisLysTrpGluThrHisLeuGlnProArgSerIleThr 100
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DB 358 CCAAA-GAAAGTGAATCATATTGACGATGGACAGTGTGGCATCCAC----- 404
QY 121 ThrLeuAspSerGlyTrpLeuThrCysGlnThrGluIleArgLeuArgIleHisTyrSer 140
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QY 141 GluLysProProValSerIleThrLysLysLysLeuLysLysSerArgPheArgValLys 160
DB 405 -----AGGTA-AAG 412
QY 161 LeuThrLeuGluGlyLeuGluGlu-----AspAspAspArgValSerProThr 177
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AUTHORS Chiang, L.W.
TITLE Nucleic acid molecules derived from rat brain and programmed cell
death models
JOURNAL Patent: WO 0131007-A 1 03-MAY-2001;
Millennium Pharmaceuticals, Inc. (US)
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